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GenCore version 4.5
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protein search, using sw model OM protein

May 10, 2002, 13:51:02; Search time 14.5 Seconds (without alignments) 798.519 Million cell updates/sec Run on:

US-09-724-583-2 Perfect score: Title:

818 1 MCSLPMARYYIIKYADQKAL.....QLTKESEPSARTKFYFEGSW 152 Sequence:

Scoring table:

Searched:

219241 seqs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

219241 otal number of hits satisfying chosen parameters:

length: 0 length: 2000000000 nimum DB seq daximum DB seq

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

beta-ketoadipate e aminopeptidase m42 N5,N10-methylenete sulfate adenylyltr ibronectin-bindin polycystic kidney antigen LEC-A - mo elastic titin - hu intrinsic factor-B ubiquitinating enz probable transamin leukotriene B4 ome sulfate adenylyltr fibronectin-bindin retrovirus-related interleukin-1 Description SUMMARIES S38373 JN0724 S23010 I55969 ICB01B A30584 JC7104 C40956 A44610 A54377 A30368 A39386 JC5646 T09456 T09456 149264 A75490 S42798 A46661 S33851 I53395 I38346 ICHU1B E75067 C69399 E71409 FOMSIA DB Length Query Match 260.5 257.5 238.5 238.5 238.5 134.5 114.5 1010.5 1010.5 1010.5 104.5 104.5 107 Score Result Š.

rece rece rece rece rece beta beta beta beta beta beta

7

C40956

Cipecies: Rattus norvegicus (Norway rat)
Ribisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomps Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A.Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami A; Reference number: A40956, MUID:91271363
A.Status: preliminary
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-178 <EIS>
A.Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929

deoxycytidylate de	Iq alpha chain C r	hypothetical prote	leukotriene-B4 20-	phosphoribosylform	aquaporin homolog	anthranilate N-hyd	IqE-binding protei	hypothetical prote	norbin - rat	replication licens	PRP8 protein homol	L-sorbosone dehydr	hypothetical prote	archaeosine tRNA-r	beta-galactosidase
B82354	S09264	T47147	S45702	A84243	T12999	T45573	EBRTMS	E96713	JC5812	S42228	T30875	F75417	T51223	н69101	S41889
7	7	7	7	7	~	7	4	7	7	-	7	7	7	7	7
a	33	355	520	700	256	450	557	929	729	892	2403	398	622	665	832
53	(-1														
8.5 53	8.4			8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.3	8.2	8.2	8.2	8.2
69.5 8.5 53	8.4	8.4						68.5 8.4					67 8.2		

ALIGNMENTS

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C; Accession: JC7104
R; Mulero, J.J.: Pace, A.M.: Nelken, S.T.: Loeb, D.B.; Correa, T.R.; Drmanac, R.; Ford Biochem. Biophys. Res. Commun. 253, 702-706, 1999
A; Title: ILJHYI: A novel interleukin-1 receptor antagonist gene.
A; Reference number: JC7104; MuID:99443727
A; Receile type: mRNA
A; Molecule type: mRNA
A; Residues: 1-155 < MuL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
3
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                        C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 KVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILGVQGGSQCLSCGVGQE- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                           Length 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       34.6%; Score 283; DB 2;
45.7%; Pred. No. 8.3e-22;
ive 20; Mismatches 49
interleukin-1 receptor antagonist - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 LPENGGWNAPITDFYFQQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137 ESE----PSARTKFYFEQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                  A; Map position: 2q14
C; Keywords: macrophage
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A,Gene: 1L-1rn
A,Introns: 40/2; 70/1; 107/3
C,Superfamily: interleukin-1
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Matches 60;
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A; Rosidues: 1.178 <RES>
A; Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
B; Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A; Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat A; Reference number: 152970; MUID:94271931
A; Reference number: 152970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-1 receptor antagonist precursor - mouse
N;Alternate names: IL-IRa
C;Species: Was musculus (house mouse)
C;Species: Was musculus (house mouse)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: A44610; B40956; A49031; 156106; 152970
R;Matsushime, H: Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A;Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophag A;Reference number: A44610; MUID:91316273
A;Accession: A44610
A;Accession: A44610
A;Residues: 1-178 <AAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R;Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: A;Reference number: A40956; MUID:91271363
A;Reference number: A40956
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R;Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
Lut. J. Immunol. 21, 2775-2780, 1991
Aitle: Cloning, heterologous expression and characterization of murine interleukin eference number: A49031; MUID:92037824
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A; Residues: 23-178 <SHU>
A; Residues: 23-178 <SHU>
A; Cross-references: GB: S64082; NID: 9238584; PIDN: AAB20265.1; PID: 9238585
A; Cross-references: GB: S64082; NID: 9238585
A; Experimental source: peritoneal macrophages, ICR strain
A; Note: sequence extracted from NCBI backbone (NCBIN: 64082, NCBIP: 64085)
B; Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A; Title: Mouse IL-I receptor antegonist protein: Molecular characterization, A; Reference number: 156106; MUID: 91250712
                                                                                                                                                                                                                                                                                                                                                                                                           75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                               16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
                                                                                                                                                                                                                                                                                   45 NOKTFYLRNNQLIAGYLQGPNTKLEEKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C;Genetics:
                                                                                                                                                                                     7;
                                                                                                                           Length 178;
                                                                                                                                                                                        Indels
                                                                                                                                                                                     53;
                                                                                                                              DB 2;
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                       31.8%; Scot. No. 2c. 44.5%; Pred. No. 2c. 've 16; Mismatches 've 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TK-ESEPSARTKFYFEQ 150
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                                                                                                                                                           Local Similarity 44.5%
nes 61; Conservative
                                      C; Keywords: cytokine receptor
         C; Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 7-178 <EIS>
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Best Local S
Matches 61
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interleukin-1 receptor antagonist secreted form precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 06-0ct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C;Accession: A54377; I46729
R;Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M. A;Title: Chem. 269, 6962-6971, 1994
A;Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional ch. A;Reference numbor: A54377; MUID:94165101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                          4;
C:Keywords: cytokine receptor
C:Keywords: cytokine receptor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWP 118
                                                                                                                                                                                                                                                                                                                                               EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
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                                                                                                                                                                                                                                          74
                                                                                                                                                                                                                                                                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE
                                                                                                                                                                                                                                                                                              45 NOKTFYLRNNOLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.5%; Score 241; DB 2; Length 177; 39.2%; Pred. No. 2e-17; Live 22; Mismatches 57; Indels 1
                                                                                                                                   DB 2;
                                                                                                                                31.5%; Score 257.5; DB 2
44.5%; Pred. No. 4.1e-19;
iive 16; Mismatches 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TK-ESEPSARTKFYFEQ 150
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Best Local Similarity
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C.Superfamily: interleukin-1
C.Keywords: alternative splicing; cytokine receptor
C:Keywords: alternative splicing; cytokine receptor
F:1-180/Product: interleukin-1 receptor antagonist, short intracellular splice f
F:1-3,25-180/Product: interleukin-1 receptor antagonist,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Cross-references: EMBL:X84348; NID:91008970; PIDN:CAA59087.1; PID:91008971
R;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.
A;Title: CDNA cloning of an intracellular form of the human interleukin 1 receptor an A;Reference number: A39386; MUID:91219436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Manto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rimuzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Manto J. Exp. Med. 182, 623-628, 1995
J. Exp. Med. 182, 623-628, 1995
A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor A;Reference number: 137893; MUID:95355865
A;Accession: 137893
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 receptor antagonist, long intracellular splice form - human N;Contains: interleukin-1 receptor antagonist, short intracellular splice form C;Species: Homo sapiens (man) C;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000 C;Accession: I37893; A39386
                                                                                                                                                                                        75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                         47 NOKTEYLRNNQLVAGYLQGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 EGPSLQLEDVNIEELYKGGEEATRFTFPQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292 C:Comment: For an alternative splice form, see PIR:A30368
16 DOKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE
                                                      DB 2; Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : |||||::
| 159 TNMPDEGVMVTKFYFQE 175
                                                                                                                                                                                                                                                                                                                                                                                     135 TKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 TKESEPSAR-TKFYFEQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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A; Residues: 1-3,25-180 <HAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A39386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
                                                                                 Db
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A; Residues: 1-177 < CARA
A; Reference of this sequence, including the amino end of the mature protein, were conf
R; Elsenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
R; Elsenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
A; Title: Primary structure and functional expression from complementary DNA of a human is
A; Reference number: S08160; MUID:90136921
A; Status: not compared with conceptual translation
A; Status: not compared with conceptual translation
A; Residues: 1-177 < EL2.
A; Cross-references: GB:X52015; NID:932576; PIDN:CAA36262.1; PIDS:932577
A; Cross-references: GB:X52015; NID:932576; PIDN:CAA36262.1; PIDS:932577
B; Hannum, C. H.; Willcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Ar
B; Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A; Reference number: S08159; MUID:90136920
A; Title: Translation: S08159
A; Molecule type: Protein
A; Molecule type: Protein
                                                C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Decies: Homo sapiens (man)
C:Decies: Homo sapiens (man)
C:Decies: Homo sapiens (man)
C:Decession: A40956; 137894; A30368; S08160; S08159; A37822
R:Elsenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.: Brandhuber, B.J.; Thompson, A71tle: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: A; Reference number: A40956; MUID:91271363
A; Reference number: A40956; MUID:91271363
A; Residues: 1-177 < EIS>
A; Residues: 1-177 < EIS>
A; Cross-references: GB:M63099; NID:9186385; PIDN:AAB41943.1; PID:9186386
B; Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, F. A; Ritle: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist gas, Reserved.
A; Reference number: 137894; MUID:92338323
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A; Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
Blenkowski, M.J.; Esssalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde, Biol. Chem. 265, 14505-14511, 1990
Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A; Reference number: A37822; MUID:90354444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Purification, cloning, expression and biological characterization of an interle
A;Reference number: A30368; MUID:90220867
A;Accession: A30368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
Residues: 1-177 < LEN
Residues: 1-177 < LEN
LICOSS-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
K; Carter, D.B.; Deibeld Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.G.; Sigu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Nature 344, 633-638, 1990
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A.Cross-references: GDB.125897; OMIM:147679
A.Map position: 2344.2 - 2344.2
A.Introns: 3942; 6941; 1064.3
C.Superfamily: interleukin-1
C.Keywords: alternative splicing; cytokine receptor; extracellular proteir F.1-25/Domain: signal sequence #status predicted <SIG> F.26-177/Product: interleukin-1 receptor antagonist #status experimental · F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Acce
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                     receptor antagonist secreted form precursor - human
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                     interleukin-1
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an

Query Match

Best Loca Matches

228

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A; Molecule type: mRNA A; Residues: 1-144. L'. 146-266 <AND> C.Comment: This protein lacks a conventional signal sequence for protein export. Clea ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive. C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphokine; macrophage; mitogen
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                                                                                                                                                                                             A. Cross-references: EMBL:X56972; NID:g1808; PIDN:CAA40293.1; PID:g1809
A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having a A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having a B;Sagan, D.R.
S. Sadagan, D.R.
A;Reference number: S43047
A;Accession: S43047
A;Molecule type: mRNA
A;Residues: 1-13, CC,15-54, KC,56-63, AC,65-144, LC,146-266 <SAR>
A;Cross-references: EMBL:X54796; NID:g1273; PIDN:CAA38566.1; PID:g1274
B;Fiskerstrand, C.; Sargan, D.
Nuclect Arids Res. 18, 7165, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Wolecule type: mRNA
A;Rosadidus: 113, °C, 15-54, ′K', 56-61, ′S', 63, ′A', 65-144, ′L', 146-266 <PIS>
A;Cross-references: EMBL:X54796
A;Note: the authors translated the codon AGT for residue 62 as Arg
R;Andrews, A. E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
R;Andrews, A. E.; Barcham, G. J.; Brandon, M.R.; Nash, A.D.
A;Title: Molecular cloning and characterization of ovine IL-lalpha and IL-lbeta.
A;Reference unaber: A61246; MUID:92120716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 155969; A24719; S13029
C;Accession: 155969; A24719; S13029
J; Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 EQKSL------VLDSPCVLKALHLPSQEMSREVVFCMSFVQGEERDNKIPVALG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 28; Gaps
DNA Seq. 1, 423-426, 1991
Affile: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
Afreference number: S23010; MUID:92119335
Afrecession: S23010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 266;
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C;Superfamily: interleukin-1
Keywords: Cytokine; immunoregulation; inflammation; lymphok;
E;114-266/Product: interleukin-1 beta #status predicted <AMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nucleotide sequence of owine interleukin-1 beta A;Reference number: $13092; MUID:91088326 A;Accession: $13092
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A;Molecule type: mRNA
A;Residues: 1-269 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:6 DQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR-
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                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-266 <SEO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: alveolar macrophage
C; Comment: This protein is a pleiotropic cytokine that mediates a variety of processes is C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag C; Comment: This protein lacks a conventional signal sequence for protein export. Cleavag C; Comment: This protein lacks a unlike interleukin lapta, unlike interleukin latpha, is interleukin interleukin. Interleukin interleukin.
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15-267/Product: interleukin-1 beta #status predicted <IL1>
F;77/Binding site: myristate (Lys) (covalent) #status predicted
                                             expression in Escherichia coli and geneticall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Accession: JN0724
R;Huether, M.J; Lin, G.; Smith, D.M.; Murtaugh, M.P.; Molitor, T.W.
Refene 129, 285-289, 1993
A;Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 h
A;Reference number: JN0724; MUID:93314975
A;Accession: JN0724
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N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: OB-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
C;Accession: S23010; S43047; S13092; B61246
R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interleukin-1 beta precursor - pig
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
                                                                                                                 A; Accession: S38373
A; Status: preliminary
A; Molecule types: DNA
A; Molecule types: DNA
A; Residues: 1.267 < VANN
A; Cross-references: EMBL: X74568; NID: 9407899; PIDN: CAA52660.1; PID: 9407900
C; Genetics:
A; Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C; Superfamily: interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
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Pred. No. 2.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   r matcn 16.8%; Score 137.5; DB 2 Local Similarity 32.3%; Pred. No. 1.4e-06; nes 31; Conservative 20; Mismatches **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
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                      Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction,
A;Reference number: S38373; MUID:94039070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%; Sco
31.2%; Pre
tive 20;
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                  217, 45-52,
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es 30; Conserv
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A; Residues: 1-267 <HUE>
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Query Match Best Local S: Matches 30,

228

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RESULT

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F;114-266/Product: interleukin-1 beta #status predicted <MAT>
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                                                                                                                                                                A; Accession: A24719
A; Moblecule type: mRNA
A; Residues: 1-269 <TELD
A; Cross-references: GB: X04964; NID: 952666; PIDN: CAA28637.1; PID: 952667
B; Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McColl, A.S.; Geoghegan, K.F.; Otterness, I. FEBS Lett. 278, 98-102, 1991
A; Title: Reduction of biological activity of murine recombinant interleukin-1beta by sel A; Reference unmber: S13029; MUID: 91130610
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: 118-269 cDAU>
A;Residues: 118-269 cDAU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-lbeta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin-la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Residues: 1.266 (AML)
A. Cross-references: GB: M37211; NID:g163200; PIDN:AAA30584.1; PID:g163201
B. Leong, S. R.; Flaggs, G. M.; Lawman, M.; Gray, P.W.
Nucleic Acids Res. 16, 9054, 1988
A. Residues: 1.26180; MUID:89016591
A. Residues: 1.251, A', 253-266 (-LEO)
A. Cross-references: EMRHS. X12498; NID:9448; PIDN:CAA31018.1; PID:g449
A. Cross-references: EMRHS. X12498; NID:g448; PIDN:CAA31018.1; PID:g449
C. Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-lacka, unlike interleukin 1-alpha, is inactive.
C. Comment: Interleukin-lacka precursor is less heavily myristoylated than interleukin-lacka.
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NiAlternate names: hematopoietin-1; IL-1 beta
CiSpecies: Bos primigenius taurus (cattle)
Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1989
Accession: JU0010, 501380
Mol. Immunol. 25, 429-437, 1988
A/Filte: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin A/Reference number: A94695; MuID:88318652
A/Reference number: A94695; MuID:88318652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <1L1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATR 98
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Pred. No. 3.1e-05;
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24.4%;
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Matches 39; Conservative
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interleukin-1 beta precursor - rabbit

N.Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating
C;Species: Oryctolagus uniotlus (domestic rabbit)
C;Species: Oryctolagus uniotlus (domestic rabbit)
C;Bacies: 25-May-1989 #sequence revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; JU0082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Bjochem. Bjochys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potenti
A;Reference number: A27714; MUD:88134238
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C; Comment: This protein lacks a conventional signal sequence for protein export. Clea C; Comment: This protein lacks a conventional signal sequence for protein export. Clea C; Comment: Interleukin-lbeta, unlike interleukin lalpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin C; Superfamily: interleukin-1
C; Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen F; 117-268/Product: interleukin-1 beta #status predicted <ILB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-268 < MOR>
B; Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello
J. Immunol. 142, 2299-2306, 1989
A; Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription dur
A; Reference number: A30584; MUID:89176242
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N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
                                                                                                                                        48 RGLDR-TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
                                                                                                                                                                                      54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
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A.Molecule type: mRNA
A.Residues: 1-268 - CAN>
A.Cross.references: GB:M26295; NID:9516632; PIDN:AAA31373.1; PID:9516633
R.Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A.Title: Cloning of rabbit interleukin-1 beta: differential evolution of A.Reference number: A94230; MUID:89315718
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       Score 117; DB 1; Length 266;
Pred. No. 0.00018;
24; Mismatches 36; Indels
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   14.3%; Score 117; 29.5%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                  220 KNTVEFESVLYPNWYISTSQIEERPVFL 247
                                                                                                                                                                                                                                                                             107 GSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
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Best Local Similarity 30.6
Matches 26; Conservative
Query Match
Best Local Similarity
Matches 26; Conserv
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A. Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R.Corents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R.Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
Biochemistry 30, 2315-2323, 1991
A.Title: High-resolution three-dimensional structure of interleukin lbeta in solution A, Reference number: A44675, MUID:91159409
A, Contents: annotation; (1)H-NMR structural determination
Biol. Chem. 266, 7081-7086, 1991
A, Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a A, Reference number: A39774; MUID:91201363
A, Reference number: A39774; MUID:91201363
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A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
A; Finizel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspa
J. Mol. Biol. 209, 779-791, 1989
A; Title: Crystal structure of recombinant human interleukin-lbeta at 2.0 angstrom res
A; Feference number: A44666; MUID:90064932
A; Contents: annotation; X-ray crystallography, 2.0 angstroms
C; Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-lbeta, unlike interleukin l-alpha, is inactive.
C; Comment: Interleukin-lbeta precursor is less heavily myristoylated than interleukin
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A; Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C; Superfamily: interleukin-1
C; Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrop F:117-269/product: interleukin-1 beta #status experimenta | 7111/269/product: interleukin-1 beta #status experimenta | 7111/26/product: myristate (Lys) (covalent) (partial) #status experimental F:123/Binding site: myristate (Asn) (covalent) #status absent
     A; Reference number: A48293; MUID:93348250
A; Contents: annotation; myristylation of lysines
R; Nanduri, V. N.E.; Hullnes, J. D.; Pan, Y. C.E.; Kilian, P.L.; Stern, A.S.
Blochim. Biophys. Acta 1118, 25-35, 1991
A; Title: The role of arginine residues in interleukin 1 receptor binding. A; Reference number: S19608; MUID:92110334
A; Contents: annotation; type 1 IL-1 receptor interaction site
A; Contents: annotation of Age-120 by phenylglyoxal blocks receptor binding R; Clore, G.M.; Gronenborn, A.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Brookhaven Protein Data Bank, January 1991
A; Reference number: A50049; PDB:611B
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Best Local Similarity 29.6%;
Matches 24; Conservative
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A; Residues: 1-214 <KAT>
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A; Accession: A94023
A; Accession: A94023
A; Molecule type: mRNA
A; Moside in Fig. A; 7,7-26
A; Moside in Fig. A; 7,7-26
A; Cross references: GB: KG2770; NID: 9186268; PIDN: AAA36106.1; PID: 9307043
A; Cross references: GB: KG2770; NID: 9186268; PIDN: AAA36106.1; PID: 9307043
A; March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S. R; Mature 315, 641-647, 1985
A; Title: Cloning, sequence and expression of two distinct human interleukin-1 complement A; Reference number: A93361, MUID: 85240547
A; Accession: A93361
A; Molecule type: mRNA
A; Residues: 1-269 < MAR>
A; Residues: 1-269 < MAR>
A; Residues: Gf this sequence, including the amino end of the mature form, were confirm R; Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au A; Greence number: 121, 339-340, 1985
A; Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A; Argerence number: 151852
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R;Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, ii, S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSR 309, 1005-1008, 1989
A.;Title: [Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin A;Reference number: 138131; MUID:90249285
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A;Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic A;Reference number: A90732; MUID:88184226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: M15840; NID: 9186281; PIDN: AAA74137.1; PID: 9386816
uron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare, C. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1884
A; Title: Nucleotide sequence of human monocyte interleukin 1 precursor CDNA.
A; Reference number: A94023; MUID: 85088517
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A; Residues: 1-5, K', 7-269 <CLA>
A; Residues: 1-5, K', 7-269 <CLA>
A; Cross-references: GB:X04500; NID:933788
A; Cross-references: GB:X04500; NID:933788
A; Note: the mRNA sequence had codon AdG for 6-Lys, the DNA sequence had GAG for 6-Glu
R; Bensi, G; Raugei, G; Palla, E; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A; Title: Human interleukin-1 beta gene.
A; Reference number: A29019; MUID:87248099
A; Accession: A29019
C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E. Wucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a A;Reference number: A25542; MUID:87040762
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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-5, K<sup>2</sup>, 7-19, H<sup>2</sup>, 21-110, <sup>2</sup>, 112-176, A<sup>2</sup>, 178-213, P<sup>2</sup>, 215-269 (WEB>A; Cross-references: GB:M5493; NID:9186287; PIDN:AAA59136.1; PID:9186288
A; Cross-references: GB:M54933; NID:9186287; PIDN:AAA59136.1; PID:9186288
B; Nishida, T.; Nishino, N.; Takano, M.; Rawai, K.; Bando, K.; Masui, Y.; Nakai, Biochem. Biophys. Res. Commun. 143, 345-352, 1987
Title: CDMA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line. eference number: I55217; MUID:87156769
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R;Zsebo, K.,, Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P
Blood 71, 962-968, 1988
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A; Residues: 1-269 <NIS>
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A; Residues: 1-269 <BEN>
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Rifato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goitsuka, R.; Tsujimoto, H.; Hasegawa Gene 177, 11-16, 1996
A; A;Title: Identification of an alternatively spliced transcript of equine interleukin-A;Reference number: JC5646; MUID:97080493
A;Accession: JC5646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:D42165; NID:92463549; PIDN:BAA22528.1; PID:92463550
                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-1 beta - horse
C;Species: Equas caballus (domestic horse)
C;Date: 28-oct-1997 #sequence_revision 28-oct-1997 #text_change 20-Jun-2000
C;Accession: JC5646
                                                                                                                     54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
                                                                                                                                                         1;
   Length 269;
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      DB 1;
12.8%; Score 104.5; DB 1; 29.6%; Pred. No. 0.0035; iive 18; Mismatches 38;
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Intrinsic factor-B12 receptor Cubilin precursor - human Species: Hemo sapiens (man) Species: Hemo sapiens (man) Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000 C. Accession: T09456 F. Korstrainsen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N Blood 91, 3539-3600, 1998 A.; Itle: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
C;Comment: This protein mediates a variety of physiological response to infections and synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce C;Superfamily: interleukin-1
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A; Racession: T09456
A; Accession: T09456
A; Accession: T09456
A; Raceus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRnA
A; Residues: 1-3623 < KOZ>
A; Cross-references: EMBL:AF034611; NID:93929528; PIDN:AAC82612.1; PID:93929529
C; Genetics:
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C; Keywords: Faspal sequence #status predicted <SIG>
F; 1-34/Pomain: signal sequence #status predicted <SIG>
F; 25-3623/Product: intrinsic factor-Blz receptor #status predicted <WAT>
F; 436-467/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                            48 RGLDRT-KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
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Job time: 133 sec
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RECHORATION:

APPLICANT: Pact 3.

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APPLICATION: A NOVEL INTERLEUKIN-I RECEPTOR ANTAGONIST AND USES THEREOF TITLE OF INVENTION: A NOVEL INTERLEUKIN-I RECEPTOR ANTAGONIST AND USES THEREOF 5.

CURRENT PAPLICATION NUMBER: US/09/417,455

CURRENT FILING DATE: 1999-10-13

PRIOR PAPLICATION NUMBER: US/09/248,942

PRIOR PAPLICATION NUMBER: US/09/287,210

PRIOR APPLICATION NUMBER: US/09/287,210

PRIOR PAPLICATION NUMBER: US/09/287,210

PRIOR PAPLICATION NUMBER: US/09/287,210

PRIOR PAPLICATION NUMBER: US/09/281,370

PRIOR PAPLICATION NUMBER: US/09/281,370

PRIOR PAPLICATION NUMBER: US/09/281,89

PRIOR PAPLICATION NUMBER: US/09/099,818

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45.7%; Pred. No. 1.8e-26;
tive 20; Mismatches 49;
US-08-425-232-2
US-08-477-13-3
US-08-477-143-2
US-08-477-143-2
US-09-417-45-14
US-09-417-45-14
US-08-600-630-20
US-08-600-6300-20
US-08-17-45-30
US-09-117-45-30
US-09-113-247-16
US-09-113-247-16
US-09-113-247-16
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
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Best Local Similarity 45.7%
Matches 63; Conservative
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                                                                                                                                                              May 10, 2002, 13:50:47; Search time 12.64 Seconds (without alignments) 270.609 Million cell updates/sec
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Sequence 23, Appl
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Sequence 21, Appl
Sequence 3, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 24, Appli
Sequence 27, Appli
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                                                                                                                                                                                                                                                                       US-09-724-583-2
818
1 MCSLPWARYYIIKYADQKAL......QLTKESEPSARTKFYFEQSW 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-417-455-5
US-09-00-630C-23
US-09-017-455-10
US-09-417-455-10
US-09-417-455-9
US-09-000-630C-21
US-08-862-730C-21
US-08-862-730C-3
US-08-000-630C-3
US-08-000-630C-3
US-08-000-630C-3
US-08-000-630C-3
US-08-000-630C-3
US-08-017-455-11
US-08-177-44
US-09-131-247-2
US-09-131-247-2
US-09-131-247-2
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US-08-131-247-2
US-08-459-811-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nimum DB seq length: 0
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Perfect score:
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No.
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3: Douglas C Murdock/ Bradley, Arant, Rose & White 2001 Park Place, Suite 1400
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CURRENT FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 09/348,942
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-17
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-07-31
PRIOR FILING DATE: 1998-05-19
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                      COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,730C
FILING DATE: 5/23/97
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
                          STREET: 2001 Park Place, Suite 140
CITY: Birningham
STATE: Alabama
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: rat IL-1ra sequence
US-08-862-730C-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/09417455 Patent No. 6294655
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44.5%;
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Best Local Similarity 44.5%
Matches 61; Conservative
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       ADDRESSEE:
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US-09-417-455-10
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     76 PTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQPVRLTQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/08862730C
Sequence 23, Application US/08862730C
Patent No. 6053600
APPLICANT: Fuller, Gerald M
APPLICANT: Funler, Serald M
APPLICANT: Funler Bencoding Canine Interleukin-1 Receptor TITLE OF INVENTION: An adoptist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    APPLICANT: Fuller, Gerald M

PAPLICANT: Fuentes, Nelson L.

TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor IIILE OF INVENTION: Antagonist
                                                                                                                                                                                                                                                                                                                                                                AUDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
CITY: Birmingham
STATE: Alahama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.8%; Score 260.5; DB 3; Length 178; 44.5%; Pred. No. 1.1e-23; tive 16; Mismatches 53; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diskette, 3.50 inch, correst in compatible operating system: microsoft Windows SOFTWARE: Wordberfect 6.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/No.~-
FILING DATE:
PRIOR APPIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 35203-2736
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear ; MOLECULE TYPE: rat IL-1ra sequence US-09-000-630C-23
                                                                                                                                                                                                                ; Sequence 23, Application US/09000630C; Patent No. 6018029; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acids
                                                 137 ESE----PSARTKFYFEQ 150
                                                                                | : | |||:|
|136 LPENGGWNAPITDFYFQQ 153
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Rest Local Similarity 44.5%
atches 61; Conservative
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CORRESPONDENCE ADDRESS:
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US-09-000-630C-23
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APPLICANT: Ford, John
APPLICANT: Pace, Ann
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110,36328
                                                                                                                                                                                                                                            75 EGPSLQLEDVNIEELYKGGEEATRFTFPQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                          45 NQKTFYLRNNQLIAGYLQGPNTKLEBKIDMVP---IDFRNV--FLGIHGGKLCLSCVKSG 99
                                                        Gaps
                                                                                                          16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
     Length 178;
                                                     Indels
; Score 260.5; DB 3;
; Pred. No. 1.1e-23;
16; Mismatches 53;
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75 EGPSLØLEDVNIEELYKGGEEATRFTFPØSSSGSAFRLEAAAWPGWFLCGPAEPQOPVQL 134
                                           75 EGPSLQLEDVNIEELYKGGEEATRFTFPSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 NOKTFYLRNNOLIAGYLOGPNIKLEGKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 DQKALYTRDGQLLVGDPVADNCCAE-KICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
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US-08-862-730C-21
Sequence 21, Application US/08862730C
Sequence 21, Application US/08862730C
SENERAL INFORMATION:
APPLICANT: Fuller, Gerald M
APPLICANT: Fuentes, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fuller, Gerald M
APPLICANT: Fuller, Gerald M
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         AUDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
CITY: Birmingham
STATE: Alabama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Microsoft Windows SOFTWARE: WordOwsfeet 6.0
SUCHRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,630C FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: mouse IL-1ra sequence US-09-000-630C-21
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                ; Sequence 21, Application US/09000630C; Patent No. 6018029; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible
                                                                                                             135 TK-ESEPSARTKFYFEQ 150
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FILEMENT: FOLIAL
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FILEMENT: PEACE, AND
FILEMENT: FOLIAL
FILEMENT: FOLIAL
FUNDATION: A MOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/417,455
CURRENT FILING DATE: 1999-10-13
FRIOR PELLING DATE: 1999-07-07
FRIOR PELLING DATE: 1999-07-07
FRIOR PELLING DATE: 1999-04-05
FRIOR PELLING DATE: 1999-04-05
FRIOR PELLOR NUMBER: US 09/281,370
FRIOR PELLING DATE: 1999-01-17
FRIOR PELLING DATE: 1999-01-17
FRIOR PELLING DATE: 1999-01-17
FRIOR PELLOR NUMBER: US 09/251,370
FRIOR PELLOR DATE: 1999-01-13
FRIOR PELLOR NUMBER: US 09/251,370
FRIOR PELLOR DATE: 1999-01-13
FRIOR APPLICATION NUMBER: US 09/099,818
FRIOR PELLOR DATE: 1998-05-10
FRIOR PELLOR DATE: 1998-05-10
FRIOR PELLOR DATE: 1998-05-10
FRIOR PELLOR DATE: 1998-05-10
FRIOR PELLOR DATE: 1998-05-15
FRIOR PELLOR DATE: 1998-04-03
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Pred. No. 2.5e-23;
5; Mismatches 53; Indels 7
                                                                                                                                                                                                            DB 4; Length 178;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                            ; Score 260.5; DB 4;
; Pred. No. 1.1e-23;
16; Mismatches 53;
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 178
TYPE: PRT
TYPE: PRT
US-09-417-455-10
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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Patent No. 6294655
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Best Local Similarity 44.5%;
Matches 61; Conservative 1
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160 TNTPKEPCTVTKFYFQE 176
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Best Local Similarity 44.59
Matches 61; Conservative
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US-09-417-455-9
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APPLICANT: Ford, John
APPLICANT: Pace, Ann
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US-09-000-630C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fuller, Gerald M
APPLICANT: Fuentes, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ANIONGA C Murdock/ Bradley, Arant, Rose & White STREET: 2001 park Place, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
CITY: Birmingham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 31.2%; Score 255.5; DB 3; Best Local Similarity 44.5%; Pred. No. 4.4e-23; Matches 61; Conservative 16; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, COMPOTER: IBM compatible OPERATING SYSTEM: Microsoft Windows SOFTWARE: Wordberfect 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/000,630C FILING DATE:
                                                                                                                                                                                                SYSTEM: Microsoft Windows
WordPerfect 6.0
                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: mouse IL-1ra sequence US-08-862-730C-21
                                                                                                                                                                                                                                                       US/08/862,730C
                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM COMPatible
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APPLICATION NUMBER: 08/862,730
FILING DATE:
                                                                                                                                                                                                                                                                                           INFORMATION FOR SEG ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TK-ESEPSARTKFYFEQ 150
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APPLICATION NUMBER: US,
FILING DATE: 5/23/97
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                                                                                                                                              COMPUTER READABLE FORM:
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                                                                      Birmingham
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                                                                                        STATE: Alabama
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TOPOLOGY: lin
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                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08862730C
| Patent No. 6063600
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Fuller, Gerald M. | APPLICANT: Fuller, Gerald M. | TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor TITLE OF INVENTION: Antagonist | NUMBER OF SEQUENCES: 27 | NUMBER OF SEQUENCES: 27 | CARESPONDENCE ADDRESSE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
                                                                                                                                                                  30.3%; Score 24%; DB 3; Length 151; 39.7%; Pred. No. 2.8e-22; Live 20; Mismatches 61; Indels
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39.7%; Pred. No. 2.8e-22;
iive 20; Mismatches 61
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MOLECULE TYPE: mature peptide
US-08-862-730C-3
LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: mature peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 5/23/97
INFORMATION FOR SEQ ID NO: 3:
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amino acid
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Best Local Similarity 39.7%
Matches 60; Conservative
                                                                                                                                                                        Query Match
Best Local Similarity 39.79
Matches 60; Conservative
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CITY: Birmingham
STATE: Alabama
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ZIP: 35203-2736
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 30.3%; Score 248; DB 3; Length 154;
Best Local Similarity 39.7%; Pred. No. 2.9e-22;
Matches 60; Conservative 20; Mismatches 61; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fuller, Gerald M
APPLICANT: Fuller, Gerald M
APPLICANT: Fuller, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
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Patent No. 6063600
GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M
APPLICANT: Fuller, Nelson L.
TITLE OF INVENTION: Antagonist
TITLE OF INVENTION: Antagonist
                                                                                                                                                                                                                                              ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400 CITY: Birmingham
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: cleaved IL-1ra peptide from fusion construct "08-09-000-630C-5
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                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: WordPerfect 6.0
CUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,630C
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/862,730
                                           Sequence 5, Application US/09000630C Patent No. 6018029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
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LENGTH: 154 amino acids
TYPE: amino acid
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CITY: Birmingham
STATE: Alabama
                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 35203-2736
                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 35203-2736
                                                                                                                                                                                                                                                                                                                     Alabama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
RESULT 10
US-09-000-630C-5
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US-08-862-730C-5
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61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M.
APPLICANT: Fuentes, Melson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
CARREST: 2001 Park Place, Suite 1400
CITY: Birmingham
                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: cleaved IL-1ra peptide from fusion construct US-08-862-730C-5
                                                                                                                                                                                                                                                                                                                                                                                                              Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                        30.3%; Score 248; DB 3; Length 154
39.7%; Pred. No. 2.9e-22;
Live 20; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 248; DB 3;
Pred. No. 3.5e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Wordberfect 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM compatible OPERATING SYSTEM: Microsoft Windows SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/000,630C
                                                                                                                                                 APPLICATION NUMBER: US/08/862,730C
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09000630C
Patent No. 6018029
                                                                                                                                                                FILING DATE: 5/23/97
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.7%
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 176 amino acids
amino acid
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MOLECULE TYPE: IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 35203-2736
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DNA Encoding Canine Interleukin-1 Receptor
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APPLICATION NUMBER: US/08/862,730C FILING DATE: 5/23/97
                                                                                                                                                                                                                                                    Microsoft Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rabbit IL-1ra sequence
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/000,630C FILING DATE:
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: 08/862,730
                    Antagonist
                                                                                                                                                                                                                                                                  SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                            : 177 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 39.29
Matches 60; Conservative
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MEDIUM TYPE: Diskett
TITLE OF INVENTION: DN
TITLE OF INVENTION: AN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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                                                                                                               Birmingham
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35203-2736
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                                                                                                                                  Alabama
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TOPOLOGY: lin
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US-09-000-630C-22
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                                                                                                                                                       COUNTRY:
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    4;
                                                                                                                 61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
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    Gaps
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                                     2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                          33 CRMOAFRIWDV----PHAVFLG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 CRMQAFRIWDV----PUKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE-----PHAVFLG 84
                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08862730C
tent No. 6053600

ENERAL INFORMATION:
APPLICANT: Fuelter, Gerald M
APPLICANT: Fuelter, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor.
TITLE OF INVENTION: Antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400 CITY: Birmingham STATE: Alabama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.3%; Score 248; DB 3; Length 176; Best Local Similarity 39.7%; Pred. No. 3.5e-22; Matches 60; Conservative 20; Mismatches 61; Indels
  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: IL-lra full length peptide
  20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                              121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                       145 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Microsoft Windows SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
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Sequence 22, Application US/09000630C

Patent No. 6018029

GENERAL INFORMATION:

APPLICANT: Fuller, Gerald M

R APPLICANT: Fuentes, Nelson L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/86
FILING DATE: 5/23/97
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 176 amino acids
TYPE: amino acid
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
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  60;
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  Matches
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59 LGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFQSSSGSAFRLEAAAWP 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 CRMQAFRIWDV---NQKTFYLRNNQLVAGYLQGPNAKLEERIDVVPLE-----PQLLF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M
APPLICANT: Fuller, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
TITLE OF INVENTION: Antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
ADDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.5%; Score 241; DB 3; Le
39.2%; Pred. No. 2.5e-21;
Live 22; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 GWFLCGPAEPQQPVQLTKESEPS-ARTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 GWFLCTALEADQPVSLTNTPDDSIVVTKFYFQE 175
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SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acids
STRANDEDMESS: single
STRANDEDMESS: single
TOPOLOGY: linear
US-08-862-730C-22

QUETY MATCH
QUETY MATCH
QUETY MATCH
QUETY MATCH
QUETY MATCH
29.5%; SCORE 241; DB 3; Length 177;
Best Local Similarity 39.2%; Pred. No. 2.5e-21;
MATCHES 60; Conservative 22; Mismatches 57; Indels 14; Gaps 5;
MATCHES 60; Conservative 22; Mismatches 57; Indels 14; Gaps 6;
Db 33 CRMQARRYIKYADOKALYTROGILVGDEVADNC-CAEKICTLPURGLDRRKVP--IF 58
SIGNGGSRCIACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFOSSSGSAFKLEAAAWP 118
SIGNGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFOSSSGSAFKLEAAAWP 118
SIGNGGRCLCLSCVKSGDEMKLHLEAVNITDLGKNKEQDDKRFTFIRSNSGPTTTFESASCP 142
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May 10, 2002, 13:50:17 ; Search time 23.86 Seconds (without alignments) 471.883 Million cell updates/sec
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1 MCSLPMARYYIIKYADQKAL......QLTKESEPSARTKFYFEQSW 152
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1. (S1D88/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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3. (S1D88/gcgdata/geneseq/geneseq/geneseqp/AA1999.DAT:*
3. (S1D88/gcgdata/gene
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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dximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
		æ				
Result		Query				
No.	Score	Match	e Match Length DB	DB	ID	Description
1	818	100.0	152	22		Human FII1 thota
7	818	100.0		22	AAB19922	Himan interleukin-
٣	818	100.0	169	22	AAB19923	Human interleukin-
4	818	100.0		22	AAB19924	Human interleukin-
2	729.5	89.2		22	AAB84999	Human interleukin-
9	657	80.3		22	AAE05841	Mouse FIL-1 theta
7	657	80.3		22	AAB19925	Mouse interleukin-
80	587	71.8		22	AAE05839	Human FIL-1 theta
6	309	37.8		19	AAW86284	Rodent interleukin
10	309	37.8		20	AAY28407	Mouse interleukin
11	309	37.8		21	AAY92260	Murine II1 homolo

isolated FIL-1 theta polypeptide to induce or inhibit the induction of

WPI; 2001-457718/49. N-PSDB; AAD11148.

Sims JE;

12 309 13 307	37.8	156 154	21 22	AAY45061 AAE06663	Murine TANGO-93 pr Mouse interleukin-
	37.5	155	21	AAY96937	IL-1 rece
	37.5	155	525	AAB66672	Invention related
	35.3	155	21	AAY92256	Murine interleukin Human IL-1 homolog
	34.6	154	22	AAB35263	Interleukin-IL1 re
	34.6	155	21	AAY96936	Human IL-1 recepto
	34.6	155	21	AAY92257	Human IL-1 homolog
	34.6	155	22	AAE06655	Human interleukin-
	34.6	155	22	AAB87601	Human PRO4342. Ho
	34.6	155	22	AAB35262	numan ir ini nom Interleukin-Itl re
	34.6	155	22	AAB66664	Protein encoded by
	34.0	155	77	AAY92255	Interleukin-IL1 re Generic human II.1
	34.2	155	20	AAY43526	A human interleuki
	33.7	155	21	AAY92253	Generic human IL-1
26	31.8	125	20	AAY92254 AAY43528	Hhuman IL-1 homolo Rat interlembin-1
56	31.8	178	20	AAY33280	Rat interleukin-1
26	31.8	178	22	AAB66666	Rat interleukin-1
2.0	2 T. C	178	3 6	AAY4352/	Mouse interleukin-
25	31.5	178	2 2	AAB66665	Mouse interleukin- Mouse interleukin-
	30.3	151	20	AAW81060	Amino acid sequenc
	30.3	154	20	AAW81062	fusion protein of
	30.3	176	20	AAW81061	
	200	177	2 5	AA143323	Rabbit interleukin
24	29.4	159	16	AAR73642	kabbit interieukin iCIL-1ra. Homo sa
				ALIGNMENTS	
SULT 1 E05840 AAE05840	standard;	; Protein;		152 AA .	
AC AAE05840;					
X T 24-SEP-2001	. (first	st entry)	y)		
XX DE Human FIL-1	theta	full-length	engt	h protein.	
_	1-1 fam endent dysplas	family liganient diabetes	ligand; abetes m ; wrinkl	~ ~	E C
tibial	コ	stroph	у; і	ıflammation; gene th	
S Homo sapiens	. 8.				
PN W0200155211	-A2.				
AA PD 02-AUG-2001	•				
PF 25-JAN-2001		2001WO-US0251	514.		
PR 27-JAN-2000; PR 11-APR-2000;	; 2000US-	JS-017838 JS-019596	389. 962.		
(IMMV)	IMMUNEX CORP	ORP.			

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us-09-724-583-2.rag

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30-NOV-2000
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AAB19923
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fever and to stimulate the immune system for the treatment of microbial
                                                                                              polypeptides and nucleic acid molecules encoding such polypeptides and nucleic acid molecules encoding such polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/ lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1 theta polypeptides are used to activate and/or inhibit the activation of vascular endothelial cells and lymphocytes; the induction of local tissue destruction and fever; the stimulation of macrophages and vascular endothelial cells to produce IL-6 and the induction of prostaglandins. They are also used to treat inflammation and microbial infections. FIL-1 theta DNA is useful in antisense therapy and gene therapy. The present sequence is human FIL-1 theta full-length protein.
                                                                                   relates to interleukin-1 (IL-1) family ligand designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                             1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "polymorphism in nucleotide sequence, alters Thr-44 to 11e"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "polymorphism in nucleotide sequence, alters Asp\ensuremath{^{-5}1} to Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; mpeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 818; DB 22; Length 152; 100.0%; Pred. No. 2.4e-86; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human interleukin-1 Hy2 (short version).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19922 standard; Protein; 152 AA.
                                                 Claim 14; Page 5; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2000; 2000WO-US14144.
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10-MAR-2000; 2000US-0522964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 51 /note=
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 44
                                                                                                                                                                                                                                                                                                           152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200071719-A1.
                                                                                   invention
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                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB19922;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                              Matches
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AAB19922
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The sequence is predicted from isolated clone diese AAA89175 and AAA89176. Petential polymorphisms in the coding region may alter the sequence, specifically changing Thr-44 to ile and Asp-51 to Ala, which may affect the biological activity of the molecule. An alternative, extended open reading frame encodes a 200-amino acid protein (see AAB19924). IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of bone, acute myelogenous leukeemia, oral epidermoid carcinoma or
                                                                                                                                                                                                                             ed polynucleotide encoding interleukin-1 Hy2 for diagnosing, and treating disorders, such as cancers and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence is that of human interleukin-1 Hy2 (IL-1 Hy2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             squamous cell carcinoma, and inflammatory disease mediated by squamous cell carcinoma, and inflammatory disease mediated by interleukin-18 (all claimed). They can also be used to diagnose, prevent or treat shock, thrombosis, acute pancreatitis, arthritis, vasculitis, lupus, immune complex glomerulonephritis, pancreatic cell damage, allograft and xenograft transplantation, graft versus host disease, inflammatory bowel disease, bone degenerative diseases, diabetes and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy.
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0
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                                                                  Pace AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 818; DB 22; 100.0%; Pred. No. 2.4e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 130-132; 158pp; English.
                                                              Lin HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB19923 standard; Protein; 169 AA.
                                                                  Ho AS,
                                                                                                                                                                  N-PSDB; AAA89175, AAA89176.
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Best Local Similarity 100.
Matches 152; Conservative
                                                                  'n,
                                                                  Ford
                                                                                                                                WPI; 2001-016409/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 AA;
(HYSE-) HYSEQ INC.
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                                                                  Ballinger DG,
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                                                                                                                                                                                                                                        New isolated
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                                                                                                                                                                                                                                                                     preventing
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Mon May 20 10:15:14 2002

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WO200071719-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases
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ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a human interleukin-1 Hy2 (IL-1 Hy2)

Conorfull length polypeptide, as predicted from an isolated cDNA clone (See AAAB9175). A 200-amino acid full-length sequence is given in AAB1994. IL-1 Hy2 is a novel member of the interleukin-1 receptor antagonist family. IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or squamous cell carcinoma, and inflammatory disease mediated by interleukin-18 (all claimed). They can also be used to diagnose, prevent or treat shock, thrombosis, acute pancreatitis, arthritis, vacultiis, lupus, immune complex glomerulonephritis, pancreatic cell damage, allograft and xenograft transplantation, graft versus cost disease, inflammatory bowel disease, bone degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing, preventing and treating disorders, such as cancers and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor; antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 818; DB 22; Length 169; 100.0%; Pred. No. 2.7e-86; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                        Pace AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Page 134-145; 158pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB19924 standard; Protein; 200 AA
                                                                                                                                                                                                                                        Ho AS,
                            22-MAY-2000; 2000WO-US14144.
                                                                                  20-MAY-1999; 99US-0316086.
10-MAR-2000; 2000US-0522964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100,0
Matches 152; Conservative
                                                                                                                                                                                                                                        J,
                                                                                                                                                                                                                                                                                              WPI; 2001-016409/02.
                                                                                                                                                                                                                                 Ballinger DG, Ford
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                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA89175
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The present sequence is that of human interleukin-1 Hy2 (IL-1 Hy2), a novel member of the interleukin-1 receptor antagonist family. The sequence is predicted from the genomic DNA sequence (see AAA89177) and a predicted CDNA sequence (see AAA89177) and a predicted CDNA sequence (see AAA89178). An alternative open reading frame (see AAA89176) encodes a 152 polypeptide (see AAA89922). IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, glant cell tumours of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or squamous cell carcinoma, and inflammatory disease mediated by interleukin-18 (all claimed). They can also be used to diagnose, prevent or treat shock thrombosis, acute pancreatitis, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing, preventing and treating disorders, such as cancers and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vasculitis, lupus, immune complex glomerulonephritis, pancreatic cell damage, allograft and xenograft transplantation, graft versus host disease, inflammatory bowel disease, bone degenerative diseases, diabetes and neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human interleukin-1 receptor antagonist (NOVINTRA A) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 818; DB 22; Length 200; 100.0%; Pred. No. 3.4e-86; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                               Pace AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 flcgpaepgqpvqltkesepsartkfyfeqsw 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Page 144-145; 158pp; English.
                                                                                                                                                                                                                                                                                                                           Lin HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
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                                                                                                                                                                                                                                                                                                                           Ho AS,
                                                                                                                                            20-MAY-1999; 99US-0316086.
10-MAR-2000; 2000US-0522964.
                                                                      22-MAY-2000; 2000WO-US14144
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA89177, AAA89178.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                           Ford J,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-016409/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AA;
                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                       Ballinger DG,
                                                                                                                                            20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-2001
30-NOV-2000
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Mus musculus.
                                                                                                                                                                                                                                                                                                                        27-JAN-2000;
                                                                                                                                                                                                                                                        32-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  Sims JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB19925
ID AAB19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention provides novel polypeptides (NOVX) selected from human transmembrane protein (NOVERAN), neuromedin peptide (NOVERR), canadorized protein (NOVERAN), neuromedin peptide (NOVERR), gonadotropin-like protein (NOVERAN), neuromedin peptide (NOVERR), mentagonist proceins (NOVINTRA A and B). The invention also provides cantagonist proceins (NOVINTRA A and B). The invention also provides the those in which a NOVY ROI ypeptide, polynuclectide and antibody are used in the detection, prevention and treatment of a broad range of pathological states. NOVTRAN can be used to treat is a cell signaling disorder, enurodegenerative disorder, neurodegenerative disorder, neurologic disorder, cancers of central nervous system, breast, colon, ovary, kindrey, prostate and thyroid. NOVGON can be used to treat reproductive development disorder, metabolic function disorder and melanoma. NOVINTRA A and B can be used to treat bone metabolism or structure disorder, inflammantory response disorder, immune regulation disorder, septic shock, stroke, diabetes, arthritis and cancer. The present sequence represents the NOVINTRA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 ETEEGPSLOLE-----DVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zerhusen BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated human transmembrane, neuromedin peptide gonadotropin-like protein and interleukin-1 receptor antagonist proteins, useful for treating cancer, immune response disorder, metabolic function disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 729.5; DB 22; Length
Pred. No. 3.8e-76;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                     Rastelli L,
                                                                                                                                                                                                                                                                                                     Burgess CE, Prayaga SK, Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAEPQQPVQLTKESEPSARTKFYFEQSW 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE05841 standard; Protein; 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 9B; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%;
93.9%;
                                                                                                                                                                         99US-0169866.
99US-0169886.
99US-0170252.
2000US-0175740.
antiasthmatic; antiallergic.
                                                                                                                            2000WO-US33029
                                                                                                                                                         99US-0169056
                                                                                                                                                                                                                                       2000US-0170252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 93.9
Matches 139; Conservative
                                                                                                                                                                                                                                                                        CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-374790/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF83868
                                                              WO200140291-A2
                                Homo sapiens.
                                                                                                                            06-DEC-2000;
                                                                                                                                                                         09-DEC-1999;
09-DEC-1999;
10-DEC-1999;
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                                                                                                                                                                                                                         12-JAN-2000;
                                                                                                                                                         06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide.
                                                                                           07-JUN-2001
                                                                                                                                                                                                                                                                                                                        Wezes PS;
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ID AAE0
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isolated FIL-1 theta polypeptide to induce or inhibit the induction of ever and to stimulate the immune system for the treatment of microbial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                  Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia; insulin dependent diabetes mellitus; lymphoma; microbial infection; ectodermal dysplasia; wrinkly skin syndrome; antisense therapy; tibial muscular dystrophy; inflammation; gene therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
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82.1%; Pred. No. 8.5e-68;
ive 10; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0178389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000; 2000US-0195962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001; 2001WO-US02514.
24-SEP-2001 (first entry)
                                                                    Mouse FIL-1 theta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.18
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457718/49.
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isolated FIL-1 theta polypeptide to induce or inhibit the induction of fever and to stimulate the immune system for the treatment of microbial infections -
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                                                                                                                                      Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia; insulin dependent diabetes mellitus; lymphoma; microbial infection; ectodermal dysplasia; wrinkly skin syndrome; antisense therapy; tibial muscular dystrophy; inflammation; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 4; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000US-0195962.
                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2001; 2001WO-US02514.
                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0178389
                                                      (first entry)
                                                                                              Human FIL-1 theta protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-457718/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD11147
                                                                                                                                                                                                                                                                                             WO200155211-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-2000;
                                                   24-SEP-2001
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           AAE05839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sims JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing, preventing and treating disorders, such as cancers and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of mouse interleukin-1 Hy2 (IL-1 Hy2), as predicted from the genomic DNA sequence (see AAA89179). IL-1 Hy2 as a novel member of the interleukin-1 receptor antagonist family. The predicted mouse and hunan (see AAB19922) IL-1 Hy2 polypeptides share 81.7% homology. Murine genomic DNA can be used to generate transgenic animals which overexpress IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out. Human IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor; antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or squamous cell carcinoma, and inflammatory disease mediated by interleukin-18 (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.3%: Score 657; DB 22; Length 152; 82.1%; Pred. No. 8.5e-68; Live 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pace AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          flcgpaepqqpvqltkesepsthtefyfems 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 9; Page 152-153; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FLCGPAEPQQPVQLTKESEPSARTKFYFEQS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE05839 standard; Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ho AS,
                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2000; 2000WO-US14144.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1999; 99US-0316086.
10-MAR-2000; 2000US-0522964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-016409/02.
N-PSDB; AAA89179, AAA89180.
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                    Mouse interleukin-1 Hy2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA;
                                                                                                                                                                                                                                                                                                      WO200071719-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ballinger DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                30-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124;
AAB19925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                            Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
AAE05839
ID AAE05
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                                                                                                                                                                                                                                                                                                        41 KICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFT 100
                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQSW 152
                        Length 112;
                                                                                                                                                                    Indels
        Score 587; DB 22;
Pred. No. 6.7e-60;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodent interleukin (IL)-1 delta polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW86284 standard; Protein; 156 AA.
71.8%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Query Match 71.8
Best Local Similarity 98.2
Matches 110; Conservative
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This represents a rodent interleukin (IL)-1 delta polypeptide. The invention relates to a recombinant polypeptide that specifically binds polyclonal antibodies (Abs) generated against a 12 consecutive amino acid segment of IL-1 delta or IL-1 depsilon. Agonists or antagonists of these IL polypeptides are used to regulate a cell involved in an inflammatory response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are used to regulate a cell involved in an inflammatory response. The IL-1 delta or IL-1 epsilon polypeptides and peptides and expected the number system, and can be used to diagnose and treat conditions associated with espilon polypeptides are used with agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are used with agonists or antagonists of IL-1 delta or IL-1 (IRA, IL-1 beta, IL-1 gamma, IL-2 and/or IL-12. The IL-1 delta or IL-1 epsilon polypeptides may be used as a soluble polypeptide or as a fusion protein with another cytokine or chemokine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
                            inflammatory response; immune system; diagnosis; agonist; antagonist; chemokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 mmvlsqalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60
             Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                               Mammalian interleukin 1-delta and 1-epsilon – useful for, e.g. regulating the immune system and inflammatory responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.8%; Score 309; DB 19;
45.2%; Pred. No. 1.1e-27;
Live 23; Mismatches 56;
                                                                                                                                                                                                                                                                                                              Sana TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kastelein RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Pages 89-90; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY28407 standard; Protein; 156
                                                                                                                                                                                                                        97US-0055111.
97US-0837627.
                                                                                                                                                                                      98WO-US06879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse interleukin 1 delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                            Bazan JF, Hedrick JA,
                                                                                                                                                                                                                                                                            (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uery Match
est Local Similarity
                                                                                                                                                                                                                                                                                                                                                WPI; 1998-609976/51.
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV71958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-1999
                                                                                                                    W09847921-A1
                                                                                                                                                                                        17-APR-1998;
                                                                                                                                                                                                                          06-AUG-1997;
                                                                                                                                                                                                                                          21-APR-1997;
                                                                                                                                                      29-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY28407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                      Wus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The present sequence represents mouse interleukin 1 delta (IL-1 delta).

IL-1 delta proteins are useful for the determination of the molecular weight of a sample protein. The protein and its fragments are useful as controls for peptide fragmentation. This 1s useful for determining the controls for peptide fragmentation. This 1s useful for determining the isoelectric point of a sample protein. Antibodies generated against II-1 delta and its fragmented peptides can be used to enhance the apparent molecular wight markers to determine the apparent molecular eight and isoelectric point of a sample protein. IL-1 delta conter-structure molecules. IL-1 delta associated with IL-1 delta counter-structure molecules. IL-1 delta associated of as therapeutic agents for the treatment of diseases mediated by IL-1 delta may be used as a reagent in studying the interleukin 1 celts. IL-1 delta may be used as a reagent to block IL-1 signalling. The IL-1 delta coding sequences can be used to identify human chromosome 2, and to identify pathway, or as a reagent to block IL-1 signalling. The IL-1 delta coding sequences can be used to identify human chromosome 2, and to identify genes associated with certain diseases, especially with region 2411-12, including glaucoma, ectodermal dysplasia, insulin-
IL-1 delta coding sequences can be used to identify human and tibial muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
Interleukin 1 delta; IL-1 delta; glaucoma; ectodermal dysplasia; insulin-dependent diabetes mellitus; wrinkly skin syndrome; T-cell leukemia; lymphoma; tibial muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine and Human interleukin 1 delta DNA, polypeptides and its fragments, useful as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.8%; Score 309; DB 20;
45.2%; Pred. No. 1.1e-27;
tive 23; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 WFLCGPAEPQOPVQLTKESEPSA----RTKFYFEQ 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 67; 72pp; English.
                                                                                                                                                                                                                                           98US-0087393.
98US-0071074.
                                                                                                                                                                                                       99WO-US00514.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 37.89
Best Local Similarity 45.29
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-458310/38.
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX89431
                                                                                                                                                                                                                                              01-JUN-1998;
09-JAN-1998;
                                                                                     Mus musculus
                                                                                                                                                                                                       38-JAN-1999;
                                                                                                                                                                  15-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY92260;
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                                                                                                                                                                                                                                                                                                                                                Sims JE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92260
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AAY45061 standard; Protein; 156 AA.

(first entry)

31-MAY-2000

AAY45061;

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C be probe generated from the DNA sequence by PCR using AAA09199-200 was used to analyze human northern blots.

C used to analyze human northern blots.

It is believed that zilla3 acts through IL-1 receptors. In general, c illa3 proteins having a Lys residue at position 148 will have anti-inflammatory activity (e.g. AAY92256). Whilst those having Asp (see AAY92254) or Glu at this position will have pro-inflammatory activity (e.g. AAY92255). Whilst those having Asp (see AAY92254) or Glu at this position will have pro-inflammatory disease such as remnance response in an animal c crion. Zilla3 is used to modulate an immune response in an animal c chronic inflammatory diseases uch as rheumatoid arthritis, costeoarthritis and Lyme arthritis, sporiasis, to reduce tissue damage after ischemia, to treat septic shock, graft-versus-host disease and creatise including crohn's disease and ulcerative colitis, insulin-dependent colluding crohn's disease and ulcerative colitis, insulin-dependent colludentes mellitus, acute pancreatitis, glomerulonephritis and cerebral schemia. Agonist forms of zilla3 may promote wound healing by IL-1 creat infections, especially gastrointestinal infections. They may also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins useful for treatment of inflammatory conditions such as rheumatoid arthritis and psoriasis are agonists or antagonists forms of
                                                         Generic; interleukin-1; IL-1; homologue; zilla3; anti-inflammatory; antagonist; pro-inflammatory; agonist; immunomodulator; antiarthritic; antirheumatic; osteopathic; antipsoriatic; antibacterial; cytostatic; immunosuppressive; antiulcer; antidiabetic; nephrotropic; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 59-60; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheppard PO, West RR, Clegg CH;
                   Murine IL-1 homologue, zilla3.
                                                                                                                                                                                                                                                                                                                                  99WO-US23533.
                                                                                                                                                                                                                                                                                                                                                                          98US-0169745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new interleukin-1 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-303780/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA09198
                                                                                                                                                      vulnerary; 2q14.
                                                                                                                                                                                                                                       WO200020595-A1.
                                                                                                                                                                                                 Mus musculus.
                                                                                                                                                                                                                                                                                                                               08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                          38-OCT-1998;
                                                                                                                                                                                                                                                                                    13-APR-2000.
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Sequence 156 AA;

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3,
                                                                                                    60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
                                                                                                                   1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
                               Gaps
                              . 9
     Length 156;
                              Indels
37.8%; Score 309; DB 21;
45.2%; Pred. No. 1.1e-27;
live 23; Mismatches 56;
                                                                                                                                                     120 WFLCGPAEPQQPVQLTKESEPSA----RTKFYFEQ 150
                                                                                                                                                                 Best Local Similarity 45.29
Matches 70; Conservative
 Query Match
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RESULT 12 AAY45061

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The present sequence is the murine TANGO-93, a secreted protein, that belongs to the gytokine superfamily. It plays a role similar to secreted interleukin-1 receptor antagonist (IL-1ra) and lits expression is developmentally regulated in liber, heart and bone marrow. TANGO-93 conditions mediated inflammation and IL-1 gene or protein expression. TANGO-93 is useful as a modulating agent for regulating expression. TANGO-93 is useful as a modulating agent for regulating expression. TANGO-93 is useful as a modulating agent for regulating expression. TANGO-93 is useful as a modulating agent for regulating cellular processes like asthma, graft vs-host disease, rheumatoid arthritis, psoriatais, inflammatory bowel disease, especie shock, ulcerative colitis, Crohn's disease, osteoarthritis, Lyme disease, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme disease, cachexia, and autoimmune diseases e.g. mysathenia gravis, autoimmune disease and systemic lupus erythematosus. Partial TANGO-93 sequences are useful as hybridisation probes and primers, for isolation sequences are useful as hybridisation probes and primers, for isolation of TANGO-93 sequence and for the creation of transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3,
                                                                                                                                                                       TANGO-93; cytokine; mouse; secreted protein; IL-1 expression; cancer; interleukin-1 receptor antagonist; IL-1ra; inflammation; antiasthmatic; immunosuppressive; antirhematic; antiarthritic; antipsoriatic; asthma; antiinflammatory; antibacterial; antialcer; cytostatic; immunomodulator; osteopathic; dermatological; antidiabetic; psoriasis; ulcerative colitis; graft vs host disease; rhemmatoid arthritis; inflammatory bowel disease; septic shock; cachexia; Crohn's disease; chronic myelogenous leukaemia; liver disease; misasthematorid arthritis; inflammatory bowel disease; autoimmune disease; myasthemia gravis; pharmacogenomic; diagnosis; systemic lupus erythematosus; forensic; transgenic animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid sequences encoding TANGO-93 polypeptide useful for treating a variety of cellular processes e.g. asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 mmvlsgalcfrmkdsalkvlylhnnqllagglhaekvikgeeisvvpnraldaslspvil 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US17886.
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Matches 70; Conservative
                                                                                                                              Murine TANGO-93 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB: AAZ50811
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77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
16 kvlylhnnqllagglhaekvikgeeisvvpnraldaslspvilgvqggsqclsc-gtekg
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IL-ldelta and IL-lepsilon are useful for treating conditions exhibiting abnormal expression of the interleukin such as immunological disorders, tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis, tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis, tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis, allergy, autoimmune diseases and infectious diseases (e.g., pulmonary tuberculosis, leprosy, fulminant hepatitis, and viral infections such as the production also relates to methods of using the composition containing IL-ldelta or IL-lepsilon for both diagnostic and therapeutic utilities. IL-ldelta is used as an immunogen for the production of antisera or antibodies specific, e.g., capable of distinguishing between IL-l family members and an IL-ldelta, for the interleukin or its frament. The purified interleukin is used as a reagent to detect any frament. The prified in response to the presence of elevated levels of expression, or immunological disorders which lead to antibody production to the endogenous cytokine. The invention also contemplates the use of competitive drug screening assays. The present sequence is mouse in interleukin-ldelta (IL-ldelta) protein related to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; interleukin-1delta; IL-1delta; virucide; hepatotropic; fever; immunological disorder; tumour; inflammatory disorder; hypoglycaemia; autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy; psoriasis; viral infection; allergy; cytokine; HIV; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated or recombinant antigenic interleukin-1 delta or epsilon polypeptide useful for treating conditions exhibiting abnormal expression of interleukin such as immunological disorders, tumor and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse interleukin-1delta (IL-1delta) protein.
                                                    120 WFLCGPAEPQOPVQLTKESEPSA----RTKFYFEQ 150
                                                                                       Bazan JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 103pp; English.
                                                                                                                                                                                                                                                                                                                                    AAE06663 standard; Protein; 154
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collected and molecule encouring an interlectant. Titre polypeptide (IL-11p) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human interleukin-1 receptor antagonist-1 (hIL-18R1) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for ecombinantly producing the IL-11p polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes (conversely, gene therapy protocols may be used to supplement a patients production of the polypeptide or to rectify mutations that lead to the production of in active peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-11p protein expression and activity which may be use to treat disorders associated with inappropriate IL-11p expression and activity, such as inflammatory disorders, asthma, arthritis, activity, such as inflammatory disorders, asthma, arthritis, syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease.
mIL-1Ra3; interleukin-1 receptor antagonist-3; IL-11p; osteopathic; interleukin-1-1ke polypeptide; anti-inflammatory; anti-asthmatic; anti-infarchoial; respiratory; anti-ischemic; vaccine; anti-iarchoial; respiratory; anti-ischemic; vaccine; dermatalogical; immunomodulatory; gastrointestinal; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated nucleic acid molecule encoding an interleukin-1-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding interleukin-1-like polypeptides, useful f
preventing and treating e.g. inflammation, asthma and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Fig 9A-B; 143pp; English.
                                                                                                                                                                                                      AAY96937 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                             Murine IL-1 receptor antagonist 3.
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99US-0116843.
99US-0129122.
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                                                           137 ESEPSA----RTKFYFEQ 150
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22-JAN-1999;
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155 AA;

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18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76

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                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; IL-ILI; interleukin-1 locus; IL-lbeta; IL-lreceptor; psoriasis; chromosome 2q13; inflammatory disease; heart disease; Graves' disease; rheumatoid arthritis; inflammatory bowel disorder; diabetes; cancer; osteoporosis; systemic lupus erythematosus.
                                                                                                            PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
                                                                                                                             6; Gaps
                                                 18 KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding human and murine interleukin-1L1 polypeptides useful for controlling inflammatory processes -
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 47.8%; Pred. No. 1.9e-27;
tive 20; Mismatches 46; Indels
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47.8%; Pred. No. 1.9e-27;
tive 20; Mismatches 46;
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                                                                                                                                                                         137 ESEPSA----RTKFYFEQ 150
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                  66; Conservative
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hes 66; Conservative
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16	5 111.6	10.9	439	12	AQ112190	AQ112190 CIT-HSP-2
1.	7 111.6	10.9	1051	11	AK009741	AK009741 Mus muscu

/gene="FKSG75"
/note="similar to ILIRN and ILIHY1"
/codon_start=1
/product="intelleukin-1 receptor antagonist FKSG75"
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TKVPIFLGIGGGSRCLACVBTEEGPSLQLEDVNIEELYKGGEBATRFTFFQSSSGSAF

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AKO08977 B1089828 B1089828 B1090567 AC55100 AC418783 AC526032 AC527034 AC624891 AC624891 AC624891 AC624891 AC624891 AC624891 AC624891 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC626032 AC636032 AC636032 AC636032 AC636032 AC636032 AC636032 AC636032 AC636033 AC636033 AC63603 AC	AQ537983 BY91215 BY165269 AU155269 AQ265967 AA194142 AQ062337 AG151628 ALIGNMENT	900 k in-1 rec 55 rordata;	J, L. teriza erijing ao Lu	Location/Qualifiers 1. :000 /organism="Homo sapiens/db_xref="taxon:9606" /chromosome="2" /map="2p14" 1. :900 /gene="FKSG75"
	700 7 77	terleucds. :128299: :128299: :120a; C	T. and chand chand chand chand chand chand chand chand 900) on (4 Tou ', 4 Tou ', 7	DN/Qualij Sm="Homc sf="taxor some="2" pl4" FKSG75" 155
11199 726 832 932 932 933 6633 705 705 705 841 841 607 607 607 607 607 607 607 607 607 607	507 594 480 483 583 4447 651	AYO26753 Homo sapiens interl MRNA, complete cds. AYO26753 AYO26753.1 GI:1282 HTC. Human. Homo sapiens BCUkaryota: Metazoa; Manmalia; Eutheria; 1 (bases 1 to 900)	Li, ion ukir to to issi 01-F Ltd.	Location/Qual 1. 900 /organism="Ho /observed = "tax, /chromosome=" /map="2214" /map="2214" /map="2214" /map="2214"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 285)
Dias Neto.F., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva, W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
                                                                                                                                                                                                                                   540 ttttagccttgtgccccaaaccaagctcatcctgctcagggtctatggtaggcagaata 599
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                                                                                                                                                                             240 ggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccct 299
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                                                                                              Gaps
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                                                                 Length 900;
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RLEAAAWPGWFLCGPAEPQOPVQLTKESEPSARTKFYFEQSW"
232 c 247 q 209 t
                                                                                             Indels
                                                                   DB 11;
                                                                 Score 714.8; DB 11
Pred. No. 1.1e-166;
0; Mismatches 2;
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             247
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BI051175.1 GI:14458705
                                                                 70.18;
99.78;
                                                                               Best Local Similarity 99.7 Matches 716; Conservative
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Tela: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
Faxisequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
(http://www.ludwig.org.br/Scripts/gethtml2.pl?tl=CM2&t2=CM2-GN0289-
100101-685-c09&t3=2001-01-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence start: 18
High quality sequence start: 18
Coation/Qualifiers
1. 285
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7. Coation/Qualifiers
//organism="Homo sapiens"
//db.xref="taxon:9606"
//done_lib=GN0289"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_liu= cmv...
/dev_stage="Adulation normal; Vector: pucl8; Site_1: Smai ; Site_2: Smai; A mini-library was made by cloning ; Site_2: Smai; A mini-library was made by cloning ; Site_2: Smai; A mini-library was made by cloning ; Site_2: Smai; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             puc18; Site_1: SmaI
                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
         O'Hare
                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. Simpson, A.J.
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                                                                                                                                                         97 (7), 3491-3496 (2000)
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                                                                                                                                 sequence tags
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Matches 277; Conserv
                                                                                                                                                            Proc. Nat
20202663
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quality sequence stop: 573.
Location/Qualifiers
1. 574
                                                                                                                                                                                                                                                                                                                                  Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 280; Conservative
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                                                          Holzman, T., Adams, M.D. and
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Homo sapiens
Bukarayota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mateller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2192 row: J column: 17
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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E-Coli DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.9%; Score 244.2; DB 1
87.3%; Pred. No. 5.3e-50;
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Location/Qualifiers
1. .589
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Best Local Similarity 87.3
Matches 267; Conservative
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                                                         AUTHORS
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/db_xref="taxon:9606"
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/clone_lib="Br0340"
/clone_lib="Br0340"
/note="Organ: breast; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
/716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mnNA and CDNA amplification were performed under low stringency conditions."

14 a 111 c 154 g 165 t
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Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 574)

Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Magai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 caaagaggttttgcaaatgtgattatgttaaggatcttgaaatgaggagacaatcctggg 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaatgcaggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctc
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68.1%; Pred. No. 2.9e-31;
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us-09-724-583-1.rst

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tctcctctagagtctccggaaggaacacagctcttgacaca---tggatttcagctcagt 939
gggccttgagccaacaaatgcaggt-gtttttagaaggtgaaaagccaagggaacggat 882
                                                                                                    Soares and M. Fatima Bonaldo.
113 c 86 g 138 t
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Unpublished (1997)
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Homo.

1 (Dases 1 to 507)

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

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Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Emartt-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayaed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/Libli at:

Www-bio.llnl.gov/Dbrp/inage/image.image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 407.

Location/Obstp/image.image.html
                                                                                                                                                         EST 01-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                                    AI889529 507 bp mRNA linear EST 01-SEP-19 wn05902.xl NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2444594 3' similar to contains MER26.tl MER26 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         587 ggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgcata 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 tgttaccatacatgtccaaagaggttttgcaaatgtgattatg---ttaaggatcttgaa 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           704 atgaggagacaatcctgggttatccttgtgggctcagtttaatcacaagaaggaggcagg 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 ATTGTCCAGGTGGCTCAATGTAATCACAGGGGTCTTTATAAAAGCAAAAGGGAGGCAGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.5%; Score 137.2; DB 9; Length 507; Best Local Similarity 64.5%; Pred. No. 1.8e-23; Matches 272; Conservative 0; Mismatches 138; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Homo sapiens"
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/clone="IMAGE:244594"
/clone=lib="NGL_CGAP_Ut1"
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adenocarcinoma, 7 pooled tumors"
/lab_host="bH108"
            146 t
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AI889529
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/note—'Cogan: pooled: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_I: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NNI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, Sates and M. Fatina Bonaldo.
459 bp mRNA linear EST 30-MAR-1999 IMAGE:2111348 3', mRNA sequence.
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 459) NOIT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                       563 aageteateetgeteagggtetatggtaggeagaataatgteeeegaaatatgteeaca 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 AAGATAAAANAACTGACCGAAGGAGATAGGCTGAGTAATGGCTCCCTCAAGATGTCCATA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tectaateecaaagatetgtgeatatgttaecataeatgteeaaagaggttttgeaaatgt 682
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Pred. No. 3.3e-21;
0; Mismatches 146; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2111348"
/clone_lib="scares_NFL_T_GBC_S1"
/lab_host="DH108"
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Hood, L.
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E 1 (bases 1 to 392).

E 1 (bases 1 to 392).

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoc, M., Tan, F., Theising, B., White, Y., Wylie, T., Washunan EST Project

Lupublished (1997)

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 314 286 1810

Fax: 315 clone is available royalty-free through LiNL; contact the IMAGE Consortium (info@image.linl.gov) for further information.

Insert Length: 715 Std Error: 0.00

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 bp mRNA linear EST 09-NOV-1997 aut 302.51 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731715 avi mRNA sequence.
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                                                                 683 gattatgitaaggatctigaaaigaggagacaaiccigggitaicciigigggcicagii 742
                                                                                                             803 taattitgaagatggagtgagggccttgagccaacaaatgcaggtgtttttagaaggtg 862
                                                                                                                                                                                                            195 TGGCTTTGAAGGCAGATGAAGGGGC-----CAAGGAATTAGGGTGGTCTCTAGAATCTG 142
                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                /clone_lib="Soares_testis_NHT"
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AQ780593 718 bp DNA linear GSS 02-AUG-1999 HS_3138_A1_B02_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138 Col=3 Row=C, DNA sequence. AQ780593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
(Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo. " 99 c 66 g 131 t
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High Throughput Sequencing Center
University of Washington
University of Mashington
University of Mashington
University of Mashington
University of Mashington
University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617 tecaeatectaatece-aagatetgtgeatatgttaecataeatgteeaaagaggttttg 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 CAGATGTGAGTAAATGAAGACTCTTGATATGAGGAGATTACCTTGGATTATCCATGTGGA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 CCCGAGGATATCTATGAGGGAAAGAGGGATGCAGGAGGTCAGAGTCGGAAAAAGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            792 taccatgcttctaattttgaagatggagtgagg----ggccttgagccaacaaatgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 847 gigitittagaaggiggaaaagccaagggaacggaitciccictagagictccggaagga
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 127.4; DB 9; Length 3 Pred. No. 4.6e-21; 0; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ780593.1 GI:5683553
                                                                                                                                                                                                                                                                                                                                                                                                                          12.5%;
11 Similarity 65.0%;
258; Conservative
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Class: BAC ends
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
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AUTHORS
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CITBL-E1-2529E8.TR CITBL-E1 HOMO sapiens genomic clone 2529E8, DNA
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1 (bases 1 to 612)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
                  Location Violalifier 17.18
1. 718
Ab_xref="taxon:9606" | Ab_xref="taxon:9606" | Ab_xref="taxon:9606" | Aclone="plate=3138 Col=3 Row=C" | Aclone="taxon:9606" | Aclone="taxon:960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 ttaccatacatgtccaaagagttttgcaaatgtgattatgttaaggatcttgaaatgag 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 GCAATTACTCTGGATATCCCCCATGAAATTGCAAGGGTCCATCAAAAAGTCAGAGAAGGA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gagacaatcctgggttatccttgt------gggctcagtttaatcacaagaagga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agtgaggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagccaagggaa
                                                                                                                                                                                                                                                                                                                                                                                                        Score 126.2; DB 12; Length 718;
Pred. No. 9.8e-21;
0; Mismatches 133; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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Other GSSs: CITBL-E1-2529E8 TF
Contact: Shaying theo, William Nierman,
Department of Bukaryotic Genomics
The Institute for Genomic Research
High quality sequence stop: 718.
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AQ356956
AQ356956.1 GI:4184129
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 62.1
Matches 239; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                           source
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                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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                         FEATURES
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δ g Qγ q δλ g δ g ó g δ qq

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AQ442721.1 GI:4554060
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                     /sex="mails" --
/cell_type="sperm"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
a 139 c 126 g 191 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 533)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 aaccaageteateetgeteagggtetatggtaggeagaataatgteeeegaaatatgte 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 AAACAATCAGATGCAGACCAATGTCACTGTTAGACAGAATAACAGATCCCCAAAGATGTC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      844 caggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacatcctaatcccaagat-ctgtgcatatgttaccatacatgtccaaagaggttttgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtgggct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 CAGCGTCTTTAAAAATGAGACAGA-GAGGCAGGAGAGTCAAAGTGATTTGATGTGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gcttcta------attttgaagatggagtgagggccttgagccaacaaatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            964 tccacaact-ataaaataataaacttgtgttattgtaaacc 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 125; DB 12;
Pred. No. 1.9e-20;
0; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2529E8"
/clone_lib="CITBI-E1"
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.3%;
Best Local Similarity 64.2%;
Matches 296; Conservative 0
                                                                                                                                                 .612
                                                                                                                                                                                                                                                                                                                                                         156
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC111 Human Male BAC Library"
86 c 122 g 160 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAATATGTTACTTTACATGGTAAAAGGGACTTTACAGATGTGATTAAGTTAAGGATCTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702 aaatgaggagacaatcctggggttatccttgtgggctcagtttaatcacaagaaggaggca 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762 ggaagggaagagtcagagagagaatggaagataccatgcttctaattttgaagatggagtg 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 GAGATAGGTACTAGGATTAAAGTCGGTAGTAGGAAATATGATAGAGA-----TT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 822 aggggccttgagccaacaaatgcaggtgtttttagaaggtggaaaggccaagggaacgga 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 TTTTCCCCTGGAATCTCTGAAAGGAACCAGCTCGCTGACATCTTGATTTTGGCCCCATAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 ctatggtaggcagaatatgtccccgaaatatgtccacatcctaatcccaag-atctgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                882 ttctcctctagagtctccggaaggaacacagctcttgacacatggatttcagctcagtga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942 cacccatttcagacttctgacctccacaactataaaaataataacttgtgttatt 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 121; DB 12;
Pred. No. 1.8e-19;
0; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GDB:7534403"
/db_xref="taxon:9606"
/clone="RPCI-11-90J12"
/clone_lib="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .526
                                       AQ318555.1 GI:4051597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%;
59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 59.3
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC ends.
  DNA sequence.
AQ318555
                                                                                                  Homo sapiens
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                                                                                 human.
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                                     VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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COMMENT
                   ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ318555
LOCUS AQ318555 526 bp DNA linear GSS 04-MAY-1999
DEFINITION RPCIl-90J12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-90J12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                    Fax: (200) 120-200.

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (infoeresgen.com). BAC end Web Server: http://www.htsc.washington.edu
Platec 692 row: N column: 8
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 621 catcctaatcccaagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaat 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 GACCGAATACCCAGAGCCTGTGAATATATACCTTCCATGGCAAAAGGGACTTTACAGAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681 gtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtgggctcag 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     788 aagataccatgcttctaattttgaagatgagtgaggggccttgagccaacaaatgca-g 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                847 gtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa--- 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 ccaagetcatcetgetcagggtetatggtaggcagaataatgteeeegaaatatgteea 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 CAAGACTCCTTGCTCTATACTTTTGTGGTAGAGAATAATGATTTCTCAAGTAT-CCAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    741 tttaatcacaagaaggaggcag------gaagggaggagagtcagagagagatgg 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 TATAATCACAAGAATACTTAAGAATGGAAGAGGCAGACAGGAGAGTCAGAGAAAGATTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 CTGCCTTTATGAGCTGGCAAAAAAAAAAAAAAAATTCTCCTCTATAGTTTCCAGAAAC 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACACACCTCCTGACACTTGATTNTAGCCCAGTAGAAATCCTTTTGCACTTCTG 532
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 533;
                                                                                                                                                                                                                                                                                                                                                                                                                      1. :533
/organism="Homo sapiens"
/organism="Homo sapiens"
/obxref="teamon:9606"
/clone="plate=692 Col=8 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 516-3887
Eax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.0%; Score 122.2; DB 12; Length Best Local Similarity 64.4%; Pred. No. 9.3e-20; Matches 269; Conservative 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 533.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                   Proc. Nat
99380589
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Best Local S
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                   JOURNAL
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                                                         COMMENT
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Gaps

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941

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SOURCE

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2. (bases 1 to 670)

Totoki, A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (02-M01-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RKREN), Genomic Sciences Center (GSC);
and Chemical Research (RKREN), Genomic Sciences Center (GSC);
1-7-22 Submirred-our_Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9114, Fax:81-45-503-9170)

Tel:81-45-503-9114, Fax:81-45-503-9170)

Tel:81-45-503-9116, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                   Part troop odytes DNA, clone: PTB-085013.R, genomic survey sequence. AG087298.1 GI:16639100 GSS. (genome survey sequence). Part troop odytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-085013.R. Bukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           903
211 CTAGAACTCGCTATGCTGCTTTGAAGGCAGATGAAGGGGC------CAAGGAATTA 158
                                                                                   98
                                                                                                                                                   844 caggtgtttttagaaggtggaaaagccaagggaacggattctcctctagagtctccggaa
                                                                  ggaacacage--tettgacacatggattteageteagtgacacecattteagaettetga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama, Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 115.8; DB 12; Length 670; Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
180 c 121 g 193 t
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                                                                                                                                                                                                                    cctccacaactataaaataataaacttgtgttatt 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-085013.R"
                                                                                                                                                                                                                                           Location/Qualifiers
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LIBRARY
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64.28;
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R.Site 2
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Matches 228;
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Best Local S
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ACCESSION
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ORIGIN
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AG087298/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pT713D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories inc., and primed with a Not I - oligo(dT) primer [5' rgrraccaatcroaaggaGGGGGGCGCCCCAATTTTTTTTTTTTTTT 3'].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 375)
Hillier, L. Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Laslen, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, Y.T., Waterston, R. and Wilson, R.
WashGrack EST Project 1997
Unpublished (1992)
                                                                                                          375 bp mRNA linear EST 04-JUN-1997 zw82d06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782699 34,47609
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. Er from Amersham
High quality sequence stop: 322.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 atggaagataccatgcttctaattttgaagatggagtgaggggccttgagccaacaaatg 843
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           408 GATTCATTTTGAACTTCTGACCTCCAAGACCATAAGAGAATAAACTGTATTTT 462
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Best Local Similarity 62.3%;
Matches 246; Conservative (
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Clones are available from Research Genetics (info@resgen.com), BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Verter, J.C.
and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3 Reverse
Class: BAC ends.
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1. 634

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    696 atcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag--- 752
                                                                                                                                   563 aageteateetgeteagggtetatggtaggeagaataatgteeeeegaaatatgteeaea 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: CIT-HSP-384F12.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Eax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
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Paysouses Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
FAX: (206) 616-3867
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://peapec.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
plate: 619 row: L column: 14
Seq primer: 77
Class: BAC ends
Class: BAC ends
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 13-MAR-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
caaatgtgattatgttaaggatcttgaaatgaggagacaatcctgggttatccttgtggg 735
                                                                                                                                 736 ctcagtttaatcacaag----aaggagg 759
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Male blood DNA was isolated from one randomly chosen donor
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EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

a 139 c 109 g 160 t 6 others
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BASE COUNT ORIGIN

5; 6; Gaps Query Match 11.2%; Score 114.6; DB 12; Length 525; Best Local Similarity 70.0%; Pred. No. 7.1e-18; Matches 224; Conservative 0; Mismatches 90; Indels 6;

δλ g

696 atcttgaaatgaggagacaatcctgggttatcctt-gtgggctcagtttaatcacaagaa 754

ggaggcaggaagg-agagtcagagagagatggaagataccatgcttctaattttgaag 813 755

142 GGAGGCAGGAGGGTCAGAGTCACAGAGACTGGAAGATGCCACGCTGTTGGCTTTGAAG 183

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931 cagctcagtgacacccattt 950 ||| || ||| |||||| 62 TAGCCACGTGAGATCCATTT 43

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Search completed: May 19, 2002, 08:44:01 Job time: 14234 sec

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May 10, 2002, 13:52:07; Search time 11.75 Seconds (without alignments) 474.302 Million cell updates/sec
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1 MCSLPMARYYIIKYADQKAL......QLTKESEPSARTKFYFEQSW 152
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Total number of hits satisfying chosen parameters: himum DB seq length: 0

100059

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_39:*

Database :

	Description	Ή	P25085 mus musculu		P26890 oryctolagus		018999 equus cabal		P26889 sus scrofa	P21621 ovis aries	P10749 mus musculu	P51745 cervus elap	P09428 bos taurus	Q63264 rattus norv	P79162 capra hircu	P14628 oryctolagus	P79182 macaca fasc	P46648 cercocebus	P48090 macaca mula	P51493 macaca neme	homo	P41687 felis silve	Q28386 equus cabal	Q20256 caenorhabdi	homo	P98161 homo sapien	mus m	<u>ھ</u>	P11365 mouse intra	Q96324 arabidopsis	homo	_	Q9hr49 halobacteri	P03975 mus musculu
SUMMARIES	ID	IL1X_RAT	IL1X_MOUSE	IL1X_PIG	IL1X_RABIT	IL1X_HUMAN	IL1X_HORSE	IL1X_BOVIN	IL1B_PIG	IL1B_SHEEP	IL1B_MOUSE	IL1B_CEREL	IL1B_BOVIN	IL1B_RAT	IL1B_CAPHI	IL1B_RABIT	IL1B_MACFA	IL1B_CERTO	IL1B_MACMU	IL1B_MACNE	IL1B_HUMAN	IL1B_FELCA	IL1B_HORSE	YPX2_CAEEL	CPF3_HUMAN	PKD1_HUMAN	THYG_MOUSE	VLCS_MOUSE	GAG_IPMA	GTH7_ARATH	KLC3_HUMAN	CPF2_HUMAN	PURL_HALN1	IGEB_MOUSE
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Gaps

16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74

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Query Match 31.8%: Score 260.5; DB 1; Length 178; Best Local Similarity 44.5%; Pred. No. 2.7e-20; Matches 61; Conservative 16; Mismatches 53; Indels 7;

P48089 macaca mula O26278 methanobact P45582 asparagus o P79340 macaca fasc P92127 glardia lam Q59179 buchnera ap O18214 caenorhabdi O9f280 streptomyce Q9dbs5 mus musculu P52983 synechocyst P29152 p genome po P21894 bombyx mori	PRT; 178 AA. ad) sequence update) sequence update) soulsT PROTEIN PRECURSOR (IL-1RA) (IL-1RN) 28896; 28896; C.; c.; sqonist is a member of the interleukin 1 squorist is a member of the in
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271 1 2 2 2 1 1 2 2 2 2 1 1 2 2 2 2 1 1 2 2 2 2 1 1 2 2 2 2 1 1 2	STANDARD; 1. 22, Created) 1. 22, Last seq 11. 22, Last seq 12. Last sed 12. Last seq 13. Last ann us (Rat). 20a; Chordata; 14. Thompson R.C. That A.R. Thompson R.C. Thompson R.C. That A.R. Thompson R.C. Thompson R.C. That A.R. Thompson R.C. Thompson R.C. Thompson R.C. That I.C. Thompson R.C.
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                                                                                                     01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Labedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;
"The mouse interleukin 1 receptor antagonist protein: gene structure
and regulation in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-91250712; PubMed-1828262; Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.; Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.; Mouse II.1 receptor antagonist protein. Molecular characterization, ene mapping, and expression of mRNA in vitro and in vivo."; J. Immunol. 146:4228-4231(1991).
    MEDLINE-91316273; PubMed-1830498; Matsushima K., Hishinuma A., Sherr C.J. Matsushime H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J. "Cloning and expression of murine interleukin-1 receptor antagonist in macrophages stimulated by colony-stimulating factor 1."; Blood 78:616-623(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91271363; Pubmed-1828896; Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P., Brandhuber B.J., Thompson R.C.; "Interleukin I receptor antagonist is a member of the interleukin I gene family: evolution of a cytokine control mechanism."; Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_FaxID=10090;
                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                               PRT;
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01-MAY-1992 (Rel. 22, Last sequ
01-NOV-1997 (Rel. 35, Last anno
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                                                                                                                                                                                                                160 TNTPKEPCTVTKFYFOE 176
                                                                                                                                                                     135 TK-ESEPSARTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine 6:1-9(1994).
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                                                                                                                                                                                                                                                                                                                                    IL1X_MOUSE
P25085;
                                                                                                                                                                                                                                                                                     RESULT 2
IL1X_MOUSE
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11-JUL-1999 (Rel. 38, Mast annotation update)
INTERLEGRIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CROSSBREED; TISSUE-Lung;
Yin J., Murtaugh M.P.;
Tin J., Murtaugh M.P.;
"Characterization of Irap in morphine treated pig.";
Submitted (MAY 1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 NOKTEYLRNNOLIAGYLOGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
84AA002A3119C024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKIN-1 RECEPTOR ANTAGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Pred. No. 5.5e-20;
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                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN.
                                                                                                                                                                                                                                                                                       PRINTS; PR00264; INTERLEUKINI.
SMART; SM00125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
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                                                                                                                                                                                                                                              Interleukin_1.
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44.5%;
     M64404, AAA39277.1;
1.132838, AAA20576.1;
M57525, AAA39278.1;
M63100; AAA39310.1;
S64082, AAB20265.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160 TNTPEEPLIVIKFYFQE 176
EMBL; M74294; AAA39309.1;
EMBL; M64404; AAA39277.1;
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                                              EMBL, L32838; AAA20576.1
EMBL, M57525; AAA39278.1
EMBL; M63100; AAA39310.1
EMBL; S64082; AAA20265.1
PIR: B40956; B40956.
PIR: A44610.
HSSP: P18510; 11RA.
MGD; MGI:96547; Illrn.
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110
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178
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Pfam; PF00340; IL1; 1.
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SEQUENCE FROM N.A. MEDLINE=90136921; PubMed=2137201;
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                                                                                                                                                                                                                   Signal
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109
177 AA;
                                                                                                                                                                                                                   Glycoprotein;
SIGNAL
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P18510;
                                                                                                                                                                                                                                                              DISULFID
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IL1X_HUMAN
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                                                                                                                                                                                                                                                                                           01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUXIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVP--IF 58
                                                                                                                                                                                                                                                     33 CRMQAFRIWDV----PHFYLRNNQLVAGYLQGPNTKLEEKIDVVPVE------PHFVF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=94165101; PubMed=7509813;

Cominelli F., Bortcolaml M., Plzarro T.T., Monsacchi L., Ferretti M.,

Brewer M.T., Eisenberg S.P., Ng R.K.;

"Rabbit interleukin-1 receptor antagonist. Cloning, expression,
functional characterization, and regulation during intestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBL_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93052512; PubMed=1427977; Goto F., Goto K., Myrata T., Ohkawara S., Takao T., Mori S., Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.; Interleukin-1 receptor antagonist in inflammatory exudate cells rabbits. Production, purification and determination of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-1 BY BINDING TO
                                                                                                                                                                                                                14;
                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL).
2114DC6119A9D5F9 CRC64;
                                                                                                BY SIMILARITY, INTERLEUKIN-1 RECEPTOR ANTAGONIST
                                                                                                                                                                                         Length 177;
                                                                                                                                                                                                              56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamada H., Mulligan R.C.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      31.3%; Score 256; DB 1;
40.5%; Pred. No. 7.8e-20;
Live 21; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunology 77:235-244(1992).
-i- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF II RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
-i- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                      177 AA.
                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                      119 GWFLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
or send an email to license@isb-sib.ch).
                             InterPro; IPR000975; Interleukin_1.
Pfam; PR0340; ILL; 1.
PRINTS; PR00264; INTERLEUKINI.
SWART; SM00125; ILL; 1.
PR0SITE; PS00253; INTERLEUKIN_1; 1.
Glycoprotein; Signal.
SIGNAL.
                                                                                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Biol. Chem. 269:6962-6971(1994).
                                                                                                                                                        20093 MW;
                   EMBL; L38849; AAA99424.1;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                    177 AA;
                                                                                                                                                                                                 Similarity
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P26890;
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Best Local Si
Matches 62;
                                                                                                                                 DISULFID
                                                                                                                                                     SEQUENCE
                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter D.B., Delbel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L., Slightom J.L., Berger A.E., Blenkowski M.J., Sun F.F., McEwan R.N., Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C., Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L., Truesdell S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.; "Purification, cloning, expression and biological characterization of wall interleukin-I receptor antagonist protein.";
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01-NOV-1990 (Rel. 16, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
1NTERELEVIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-1RAP) (IL-1RA).
ILIRA OR ILIRA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
F5BC087F097FFEAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-1 RECEPTOR ANTAGONIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57; Indels
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Pred. No. 2.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.5%; Scc. No. 2... 39.2%; Pred. No. 2... ... 22; Mismatches ... ... ... 22; Mismatches ... ... No. C.CA'
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                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000975; Interleukin_1.
Pfam; PF00340; II.1; 1.
PRINTS; PR00264; INTERLEUKIN1.
SMART; SM00125; II.1; 1.
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MEDLINE=90220867; PubMed=2139180;
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20214 MW;
                                                                                                                                                                                                                                  EMBL; 568977; AAB30093.1; -.
EMBL; M57526; AAA31374.1; -.
EMBL; D21832; BAA04860.1; -.
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nes 60; Conservative
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177
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HSSP; P18510; 11LR.
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Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F., Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.: CDNA cloning of an intracellular from of the human interleukin 1 receptor antagonist associated with epithelium.", Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
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SEQUENCE FROM N.A.

Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,

Jenkins J.K., Drong R.F. Jr.,

Arend W.P., Smith M.F. Jr.,

**Intracellular IL-1 receptor antagonist promoter: cell type-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A., Bunner D.P., Yem A.W., Delbel M.R. Jr.; "Secondary structure and topology of interleukin-1 receptor antagonist protein determined by heteronuclear three-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 26-45.
MEDLINE-90136920; PubMed=2137200;
MEDLINE-90136920;
MEDLINE-9013692020;
MEDLINE-90136920;
M
                                                                                                                                                                                                                                                                                                                                              MEDINE-91271363; PubMed-1828896; Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P., Brandhuber B.J., Thompson R.C.; "Interleukin I receptor antagonist is a member of the interleukin I gene family: evolution of a cytokine control mechanism."; Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H., Sheer D., Solari R.; "Cloning and chromosome mapping of the human interleukin-1 receptor
Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T., Hannum C.H., Thompson R.C.; 
"Primary structure and functional expression from complementary DNA of a human interleukin-1 receptor antagonist.";
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Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
Heinrikson R.L., Chosay J.G., Tracey D.E.,
"Purification and characterization of interleukin 1 receptor level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR.
MEDLINE-94320651; PubMed=8045306;
MCDLINE-94320651; PubMed=8045306;
Schorman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
Yem A.W., Deibel M.R. Jr.,
"Solution structure of human interleukin-1 receptor antagonist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonist proteins from THP-1 cells.";
J. Biol. Chem. 265:14505-14511(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and inducible regulatory regions."; J. Immunol. 158:748-755(1997).
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MEDLINE=92297633; PubMed=1534997;
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MEDLINE-92338323; PubMed=1385987;
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                                                                                                                                                                                                         Nature 343:341-346(1990).
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Cytokine 4:83-89(1992).
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REPRESENT REPRES

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                                                                                                                                                                                                                                                                                                                                                                                                          Soffientini A., Sarubbi E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH ILIR. MEDILINE-97215904; PubMed=99062194; Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E., Akson A., Bowlin T., Yanofsky S., Barrett R.W.; An ewe vytokine-receptor binding mode revealed by the crystal structure of the IL-1 receptor with an antagonist."; Nature 386:194-200(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- FUNCTION: IL-IRA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR, IL-IRA HAS NO IL-1 LIKE ACTIVITY.
-- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
                                                             S.P.,
                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=95172072; PubMed=7867645;
Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E. Akeson A., Rowlin T.L., Yanofsky S., Barrett R.W.;
Refined crystal structure of the interlenkin-1 receptor antagonist. Presence of a disulfide link and a cis-proline.";
Eur. J. Blochem. 227:838-847(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS ARE PRODUCED BY ALTERNATIVE
MEDLINE-94230368; PubMed-8175703;
Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg
Brandhuber B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERLEUKIN-1 RECEPTOR ANTAGONIST
                                                                                                                                                 "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
-:- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
-:- DATABASE: NAME=R&D Systems' cytokine source book;
www."http://www.rndsystems.com/cyt_cat/illra.html".
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SIGNAL 1 25
CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAG
                                                                                                                                                                                                     resolution.";
J. Biol. Chem. 269:12874-12879(1994).
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PRINKE; PR00264; INTERLEUKINI.
SMART; SM00125; ILL; 1.
PROSITE; PS00253; INTERLEUKIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, M55646; AAA59138.1; EMBL, M63099; AAB41943.1; EMBL, X52015; CAA35262.1; EMBL, X52206; CAA37386.1; EMBL, X64532; CAA45832.1; EMBL, W65590; AAB92268.1; EMBL, W65590; AAB92268.1; EMBL, W65590; AAB9226.1; EMBL, W65590; AAB9226.1; EMR, A30368; A30368.2; PIR, A30368; A30368; PIR, A40956; A40956; PIR, A39386; A39386; PIR, A39386; PIR, A39386; A39386; PIR, A39386; A39386; PIR, 
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                                                                                                                                                                                                                                                                                          99 DETRLOLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILIX_HORSE STANDARD, PRT; 177 AA.
018999; 077745;
15-DEC-1998 (Rel. 37, Created)
15-DBC-1999 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
                                                                                                                                                                                                                                                                     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
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SEQUENCE FROM N.A.

MEDLINE-98285942.; PubMed-9622739;

HOWARD R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;

"Cloning of equine interleukin-1 receptor antagonist and determination of its full-length cDNA sequence.";

Am. J. Vet. Res. 59:712-716(1998)

-i. FUNCTION: IL-IRA HAS NO IL-1 LIKE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPPOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
BEDLINE-37366446; PubMed=92233277;
Kato H., Ohashi T., Matsushiro H., Watari T., Goitsuka R.,
Tsujimoto H., Hasegawa A.;
Molecular cloning and functional expression of equine interleukin-1
                                                                                                                                                                   Gaps
                                                                                                                                                                                              16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
                                                                                                                                                                                                                                44 NOKTFYLRNNOLVAGYLOGPNVNLEEKIDVVPIE-----PHALFLGIHGGKMCLSCVKSG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                     N-LINKED (GLCNAC. ..) (POTENTIAL).
MEICRGLESHLITLILETHS. -> MAL (IN
INTRACELLULAR ISOFORM).
D1690776A734057 CRC64;
                                                                                                                                                                 7;
                                                                                                                              DB 1; Length 177;
                                                                                                                           29.2%; Score 238.5; DB 1; Length 40.9%; Pred. No. 5.4e-18; Live 18; Mismatches 56; Indels
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Pfam; PF00340; IL1; 1.
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PROSITE; PS00253; INTERLEUKIN_1; 1.
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SMART; SM00125; IL1; 1.
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                                                                                                                                                                                                                                                                                                                                                                           159 THMPDEGVMVTKFYFQE 175
                                                                                                                                                                                                                                                                                                                                          135 TKESEPSAR-TKFYFEQ 150
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                                                                                                                                                               Conservative
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109
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                                                                         177 AA;
                                                                                                                                            Similarity
 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILIRN OR ILIRA.
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DISULFID
CARBOHYD
VARSPLIC
                                                                         SEQUENCE
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Best Local
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IL1X_HORSE
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                                                                                                                                                                                                                                                        61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (IL-1RN)
                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vet. Immunol. Immunopathol. 62:197-208(1998).
-!- FUNCTION: IL-1FA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
-!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                             2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                         33 CKMQAFRIWDV----NOKTFYMRNNQLVAGYLQESNTKLQEKIDVVPIE-----PDALFLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-98305607; PubMed-9643454;
KITISAWA R., FUKMed T., Yamanaka H., Hagiwara K., Goto M., Obata
Yoshino T., Iwai H.;
"Enzymatic amplification and expression of bovine interleukin-1
                                                           .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-1 RECEPTOR ANTAGONIST
PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                  10;
              INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN.
                                                                                                                                   Score 238; DB 1; Length 177; Pred. No. 6.1e-18;
                                                                                                                                                                 62; Indels
                                          BY SIMILARITY.

N-LINKED (GLCNAC. . .) (PO
F -> L (IN REF. 2).

1ABC377FIFICF80B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             174 AA.
 BY SIMILARITY.
                                                                                                                                                                 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                   121 FLCGPAEPQQPVQLT-KESEPSARTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                 145 FLCTAQEADRPVSLTNKPKESFMVTKFYLQE 175
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000975; Interleukin_1.
                                       141 B
109 N
19 F
20459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00340; IL1; 1.
PRINTS; PR00264; INTERLEUKIN1.
SMART; SM00125; IL1; 1.
                                                                                                                                 29.1%;
39.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB005148; BAA31854.1;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor antagonist cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Signal.
                                       91
109
19
177 AA;
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
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                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                           IL1X_BOVIN
077482;
                                         DISULFID
CARBOHYD
                                                                      CONFLICT
                                                                                                                                 Query Match
Best Local S
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              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IRAP)
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
-!- MISCELLANGOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESECUENCE FROM N.A.
MEDLINE-91008326; PubMed-2263490;
Fiskerstrand C., Sargan D.;
Miclectide sequence of ovine interleukin-1 beta.";
Nuclectide sequence of ovine interleukin-1 beta.";
Nucleic Arcids Res. 18:7165-7165(1990).
INCELECTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES.
THYMOTON: PRODUCED BY ACTIVATED MACROPHAGES, IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INPLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                           54 KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
                                                                                                                                                                                                                                                                                                                                                              169 KIPVTLGIKGKNLYLSCVMKDNTPTLQLEDID-PKRYPKRDMEKRFVFYKTEIKNRVEFE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-92119335; PubMed-1840515; Seow H. F., Rothel J. S., David M.J., Wood P.R.; Sethel J. S., David M.J., Wood P.R.; "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA."; DNA Seq. 1:423-426(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                   PROSITE; PS00253; INTERLEUKIN_1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
PROPEP 1 114 BY SIMILARITY.
                                                                                                                                                                                                        Score 134.5; DB 1; Length 267; Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                              Indels
                                                                                                  30404 MW; 7F6B92B784D5086F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1992 (Rel. 21, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                    114 AAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 SALYPNWYISTSQAEQKPVFLGNSKGRQDITDFTME 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 AA.
                                                                                                                                                                                                                            31.2%; Pred. wo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1991 (Rel. 18, Created)
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                                                                                                                                                                                                           16.48;
                                                                                                                                                                                                                                                              30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECRETORY PROTEINS.
  SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER.
                                                                                                  115 2
267 AA;
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                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL1B_SHEEP
                                                                                                                               SEQUENCE
                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHEEP
                                                                                                                                                                                                                                                                 Matches
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  DR KW KW CS
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                                                                                                                                    4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION 6 PROLIFERATION, 6 FIBROBLAST GROWTH FACTOR ACTIVIT.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
SUBUNIT: MONOMER.
DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFLNED FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                      61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                    Gaps
                                                                                                                                                                                  2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                       31 CEMQAFRIWDV---NQKIFYLRNNQLVAGYLQGPNTKLEEKIDVVPIE-----PHTMFLG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93314975; PubMed-8325511; Huether M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.; "Cloning, sequencing and regulation of an mRNA encoding porcine interleukin.1 beta."; Gene 129:285-289(1993).
                                                                                                                                 10;
                                                                            Score 232; DB 1; Length 174; Pred. No. 2.5e-17;
                                                                                                                                 62; Indels
  19926 MW; 1E56E7F224FF851F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                            28.4%; Score 232; DB 39.1%; Pred. No. 2.5e iive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR002346; ILL_HBGF.
InterPro; IPR000375; Interleukin_1.
InterPro; IPR003502; Interleukin_1_prop.
Pfam; PF00340; ILL__propep; 1.
PRIMTS; PR00362; ILL__BGF.
PRINTS; PR00264; INTERLEUKIN1.
                                                                                                                                                                                                                                                                                                                                                                                             121 FLCGPAEPQQPVQLTK-ESEPSARTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                             143 FLCTSLEADQPVGLTNMPTEALKVTKFYFQQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M86725; AAA02584.1; -.
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECRETORY PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; JN0724; JN0724.
HSSP; P01584; 1HIB.
174 AA;
                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9823;
                                                                                                                                 59;
  SEQUENCE
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL1B_PIG
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SEQUENCE FROM N.A.
MEDIINE-87117546; PubMed-3492706;
MEDIINE-87117546; PubMed-3492706;
The murine interleukin 1 beta gene: structure and evolution.";
Nucleic Acids Res. 14:9955-9963(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                            61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                    28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   DOKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR------TKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-88229074: Pubmed-2967326; Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Matthew J.B., Covington M., Lin Y.; "Chiracterization of murine IL-1 beta. Isolation, expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-87058957; PubMed-3491144; Gray P.M., Glaister D., Chen E., Goeddel D.V., Pennica D.; "Two oiterleukin 1 genes in the mouse: cloning and expression of CDNA for murine interleukin 1 beta."; J. Immunol. 137:3644-3648(1986).
                                                                                                                                                              PROSITE; PS00253; INTERLEUKIN_1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
                                                                                                                                                                                                                                                                                                                        16.1%; Score 132; DB 1; Length 266; 25.4%; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                        44; Indels
                                                                                                                                                                                                                    Y -> C (IN REF. 2).

Q -> K (IN REF. 2).

V -> A (IN REF. 2).

P -> L (IN REF. 2).

P -> L (IN REF. 2).
                                                                                                                                                                                                         INTERLEUKIN-1 BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
13-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 AA
                                                                                                                                                                                                                                                                                                                                                      28; Mismatches
           PIR; $23010, $23010.

HSSP, PO1584, 411B.
INCEPPO: IPR002348; ILL_HBGF.
INCEPPO: IPR000975; INCELLEUKIN_1.
INCEPPO: IPR003502; INCELLEUKIN_1.
PROM: PP00340; ILL]; I.
PROM: PP00340; ILL_Propep; I.
PRINTS; PR00264; ILL_Propep; I.
SMART; SMO0125; ILL, I.
SMART; SMO0125; ILL, I.
PROSTE: PR00264; INTERLEUKINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 140:3838-3843(1988)
                                                                                                                                                                                                                                                                                30717 MW;
                                                                                                                                                                                                                                                                                                                                        Local Similarity 25.4:
es 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: ::|| |
234 YISTSQIEEKPVFL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 FLCGPAEPQQPVQL 134
                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
S13810; S13810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL1B_MOUSE
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CONFLICT
CONFLICT
SEQUENCE
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RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RA MEDLINE-9222792; PubMed=1807351;
RA van Oostrum J. Priestle J.P., Grutter M.G., Schmitz A.;

RA van Oostrum J. Priestle J.P., Grutter M.G., Schmitz A.;

RTH STRUCTION of murine interleukin-1 beta at 2.8-A resolution.";

J. Struct. Biol. 107:189-195(1991).

-I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THEMOCYTE PROLLFERRATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERRATION, & FIBROBLAST GROWTH PACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

-I- SUBUNIT: MONORER.

-I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
AMINO ENDS OF THESE PROPERINS SERVE SOME AS YET UNDEFINED FUNCTION.

-I- MINCELLANDORS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGNENT IN THE
PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS.

--- SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER

--- SECRETORY PROFEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen; 3D-structure. 1 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30931 MW; 734FA17B02ED87EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, M15131; AAA39276.1; --
EMBL; X04964; CAA28637.1; --
PIR; A24719; A24719.
PIR; A24719.
PIR; S13029; S13029.
PDB; BIIB; 15-OCT-94.
PDB; ZMIB; 31-JAN 94.
MGD; MGI:95643; IIIb.
INTERPO: IPR000348; IIIb.
INTERPO: IPR000350; INTERLEUKin.1.
Pfam; PP00340; ILI, propep; 1.
Pfam; PP02394; ILI_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00253; INTERLEUKIN_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00262; ILÎHBĞF.
PRINTS; PR00264; INTERLEUKINI.
SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1117
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269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMATH: THE STATLARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
MISCELLANBOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER.
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                                                                                                                                                                                                                                                                           86
                                                                                                             Gaps
                                                                                                                                                                 ---- LLVGDPVADNCC 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cervus elaphus (Red deer).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                       115 VCDVPIRQLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSND---
                                                                                                                                                                                                                                                                                 39 AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATR
                                                                                                          41;
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CYLOKINE: MSCOOPhage, Mitogen; Inflammatory response; Pyrogen.
PROPER
                                                      Length 269;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                           99 FTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKES 138
                                                         DB 1;
                                                                                  .3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                               216 FVFNKIEVKSKVEFESAEFPNWYISTSOAEHKPVFLGNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                 15.2%; Sco...
24.4%; Pred. No. o...
... 28; Mismatches
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PRINTS, PR00265; ILTHBGF.
PRINTS; PR00264; INTERLEUKINI.
SMART; SM00125; ILI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34, Created)
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                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECRETORY PROTEINS.
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Pfam; PF02394; IL1_pro
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                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9860;
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01-OCT-1996 (
30-MAY-2000 (
                                                            Ouer,
Best Local Similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL1B_CEREL
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                                                         Query Match
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DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLANDOUS: THE LACKY OF A SPECIFIC HYDROPHOBIC SEGNENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-89016591; PubMed-3262866;

Leong S.R., Flaggs G.M., Lawman M., Gray P.W.;

"The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";

Nucleic Acids Res. 16:9054-9054(1988).
                                                                                                                                                                                                                                                                      KVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLE 113
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IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STINULATE THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                   |:|: |||: :: |:||: :: |:||: ::|||||: ::|
168 KIPVALGIRDKNQYLSCVKKGDTPTLQLEEVD-PKVYPKRNMEKRFVFYKTEIKDTVEFE 226
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                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDITURE-88318652; PUDMED4-3261832; MEDLINE-88318652; PUDMED4-3261832; MEDLINE-88318652; PUDMED4-3261832; MEDLINE-8831867; C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D. Gillis S., Cerretti D.P.; Schoenborn of bovine interleukin 1 alpha and interleukin 1 beta complementary DNAs."; Mol. Immunol. 25:429-437(1988).

-I. FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES THYMOXYE PROLIGERATION BY INDUCING IL-2 RELEASE, B-CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                      Ϊ;
                                                                                                                                   Length 266;
                                                                                                                                                                                                      Indels
INTERLEUKIN-1 BETA.
4F40B4E6F0D9F060 CRC64;
                                                                                      Score 119.5; DB 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                        Pred. No. 2.7e 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                    114 AAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVLYPNWYISTSHPEEKPVFL 247
   266 I
30629 MW;
                                                                                                                                      14.6%;
29.6%;
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                                                                                                                                                                        Best Local Similarity 29.69
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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S01380; S01380.
   114 2
266 AA;
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P09428;
   CHAIN
SEQUENCE
                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
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InterPro; IPR002348; IL1_HBGF
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Macrophage;
Feeser W., Freimark B.D.;
Feeser W., Freimark B.D.;
Fubmitted (AdG-1992) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PRODICED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
    THYMOCYTE PROLIFERATION BY ANDICENTED IN THE INFLAMMATORY RELEASE, B-CELL
    MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
    IDENTIFIED AS ENDOGRNOUS PROGENS, AND ARE REPORTED TO STIMULATE
    THE SHILLARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
    SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

"ISOELTANEOUS: THE LACK OF A SPECTIF CHYROPOPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 RGLDR-TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                   InterPro: IPR002348; ILL_HBGF.
InterPro: IPR00375; Interleukin 1.
InterPro: IPR003975; Interleukin 1.
Pfam; PF0340; ILL; 1.
Pfam; PF0334; ILL_Propep; 1.
PRIMTS; PR00264; ILHBGF.
PRIMTS; PR00264; ILHBGF.
SMART; SM00125; ILL; 1.
PROSITE; PS00253; INTERLEUKIN1.
PROSITE; PS00253; INTERLEUKIN1; 1.
CYCKINE; MACIOPhage; Mitogen; Inflammatory response; Pyrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 117; DB 1; Length 266; 29.5%; Pred. No. 5e-05; Live 24; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A -> G (IN REF. 2).
9D1EF8F575070586 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERLEUKIN-1 BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          063264:
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 KNTVEFESVLYPNWYISTSQIEERPVFL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30774 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M98820; AAA41426.1; -. HSSP; P10749; 2MIB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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HSSP; P01584; 1HIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER (BY SIMILARITY).

DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE DAMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

MISCELLAREDUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 FVQGETSNDKIPVALGLKGLNLYLSCVMKDGTPTLQLESVDPKQ-YPKKKMEKRFVFNKI 220
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQS 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1- FUNCTION: PRODUCED BY ACTIVATED MACROHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROFIEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIEDS AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                    1 MCSLPMARYYI-IKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR----- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capra hircus (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                          PROSITE; PSO0253: INTERLEUKIN_1; 1.
Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen. PROPEP
                                                                                                                                                                                                                                                                                                                       Ouery Match 13.8%; Score 112.5; DB 1; Length 268; Best Local Similarity 23.3%; Pred. No. 0.00015; Matches 35; Conservative 31; Mismatches 55; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Takaura H., Hashimoto O., Morl Y., Tatsumi M.; "Molecular cloning and expression of caprine IL-lalpha and IL-lbeta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                INTERLEUKIN-1 BETA.
109C19EBF69C242D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INTERLEUXIN-1 BETA PRECURSOR (IL-1 BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE IL-1 FAMILY.
InterPro; IPR000975; Interleukin_1.
InterPro; IPR000975; Interleukin_1_prop.
Pfam; PF00340; ILI, 1.
Pfam; PF02394; ILI_propep; 1.
PRINTS; PR00262; ILIHBGF.
PRINTS; PR00264; INTERLEUKINI.
SMART; SM00125; ILI, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                268 IN
30644 MW;
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                                                                                                                                                                                                                                                         268 AA;
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SOUTH THE TRANSPORT OF 
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating factor of rabbit polymorphonuclear leukocytes: identification rabbit interleukin 1 beta.";
Biochem. Biophys. Res. Commun. 150:1237-1243(1988).
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Young P.R., Sylvester D.;
"Cloning of rabbit interleukin-1 beta: differential evolution of IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TKVPIFLG 60
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J. Immunol. 142:2299-2306(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
INPERLEMINIOR BETA PRECURSOR (IL-1 BETA) (LYMPHOCYTE PROLIFERATION POTENTIATING FACTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                       Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen. PROPEP 1 113 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46; Indels
                                                                                                                                                                                                                                                                                                                                                                    INTERLEUKIN-1 BETA.
59F7B39BD1D4DDA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.6%; Score 111; DB 1; 23.9%; Pred. No. 0.00021; iive 28; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 DQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGLDR-
                                                                     EMBL; D63351; BAA09675.1; -
InterPro; IPR002346; III_HBGF.
InterPro; IPR000975; Interleukin_1.
InterPro; IPR003502; Interleukin_1_prop.
Pfam; PP00340; II.1; 1.
Pfam; PP00340; II.1, 1.
PRINTS; PR00262; III_HBGF.
PRINTS; PR00261; INTERLEUKINI.
SMART; SMO0125; II.1; 1.
PROSITE; PS00253; INTERLEUKINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89176242; PubMed=2784458;
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                                                                                                                                                                                                                                                                                                                                                                                               30769 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 FLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                  266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 32; Conserv
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P14628;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                             DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION. MISCELLARENGUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER SECRETORY PROTEINS.
Protein Eng. 2:545-551(1989).

-!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
MATURATION & PROLIFERATION, F FIBROBLAST GROWTH FACTOR ACTIVITY.
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
-!- SUBUNIT: MONOMER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 INTERLEUKIN-1 BETA.
30665 MW; 55BF44DD78D1B297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.5%; Score 110.5; DB 1 30.6%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE IL-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, D21835; BAA04863.1; -.
EMBL, M26295; AAA31373.1; -.
PIR, A27714; A27714.
PIR, A30584; A30584.
PIRS, J00682, J00682.
HSSP, P01584; HIB.
InterPro; IPR002348; Interleukin.1.
InterPro; IPR00349; Interleukin.1.
Pfam; PF00340; IL1; 1.
Pfam; PF00349; IL1; Interleukin.1.
Pram; PF00399; IL1, IL1, Proper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: May 10, 2002, 13:54:03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAQFPNWYISTSQTEYMPVFLGNNS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00253; INTERLEUKIN_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0262; ILIHBGF
PRINTS; PR00264; INTERLEUKINI.
SMART; SM00125; ILI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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RESULT 1
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Copyright (c) 1993 - 2000 Compugen
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Maximum Match 100%
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ALIGNMENTS

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                                    APPLICANT: Ballinger, Dennis G.
APPLICANT: Ballinger, Ann M.
TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
FILE REFERENCE: 28110/35659
CURRENT APPLICATION NOWBER: US/09/316,081
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
; Sequence 1, Application US/09316081; Patent No. 6339141; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.77
Matches 993; Conservative
                                                                                                                                                           LENGTH: 998
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (54)..(512)
-09-316-081-1
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Sequence 1, Description

SUMMARIES

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Query Match I

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Sequence 4, Sequence 6, Requence 6, Requence 6, Requence 11, Sequence 11, Sequence 22, Sequence 22, Sequence 11, Sequence 41, Sequence 41, Sequence 41, Sequence 24, Sequence 12, Sequence 11, Sequence

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                                                                                                                                                                                                         Materials
                                                                                                                                                                                                                                                                                                                                                       97.2%; Score 991.2;
99.7%; Pred. No. 9.4e
iive 0; Mismatches
                                                                                                                                                                                                                                                                                081
                                                                                                                                                                                                                                                          APPLICANT: Ballinger, Dennis G.
APPLICANT: Pace, Ann M.
TITLE OF INVENTION: Interleukin-1 Hy2 Mathrice Reference: 28110/35659
CURRENT APPLICATION NUMBER: US/09/316,087
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                            Sequence 3, Application US/09316081 Patent No. 6339141 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (3)..(512)
US-09-316-081-3
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Best Local Similarity
Matches 993; Conserv
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                      coctococatggcaagatactacataattaaatatgcagaccagaaggctctatacacaa
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US-09-417-455-4
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Sequence 4, Application US/09348942
Patent No. 6337072
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Best Local Similarity 58.6
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: HOMO sapiens
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US-09-348-942-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
US-09-348-942-4
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                             ### PPPLICANI'S PACE, AND

TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF

FILE REPERENCE: 28110/36328

GURRENT APPLICATION NUMBER: US/09/417,455

CURRENT PILING DATE: 1999-01-13

PRIOR FILING DATE: 1999-07-07

PRIOR PLICATION NUMBER: US 09/287,210

PRIOR PLICATION NUMBER: US 09/251,370

PRIOR PLICATION NUMBER: US 09/251,370

PRIOR PLICATION NUMBER: US 09/251,370

PRIOR PLICATION NUMBER: US 09/259,591

PRIOR PLICATION NUMBER: US 09/229,591

PRIOR PLICATION NUMBER: US 09/229,591

PRIOR PLICATION NUMBER: US 09/229,591

PRIOR PLICATION NUMBER: US 09/099,818

PRIOR PLICATION NUMBER: US 09/099,818

PRIOR PLICATION NUMBER: US 09/099,818

PRIOR PLICATION NUMBER: US 09/092,364

PRIOR PLICATION NUMBER: US 09/055,010

PRIOR PLICATION NUMBER: US 09/055,010

PRIOR PLING DATE: 1998-04-03

NUMBER OF SED ID NOS: 30

SED ID NO 4

SED ID NO 4

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SED ID NO 4
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (73)...(537)
US-09-417-455-4
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GENERAL INFORMATION:
APPLICANT: John Ford
TILLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 2810/35801
CURRENT APPLICATION NUMBER: US/09/348,942
CURRENT FILING DATE: 1999-004-05
EARLIER APPLICATION NUMBER: US 09/287,210
EARLIER FILING DATE: 1999-04-05
EARLIER PELLING DATE: 1999-01-13
EARLIER PELLING DATE: 1999-01-13
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-05-10
EARLIER PELLING DATE: 1998-05-10
EARLIER PELLING DATE: 1998-05-10
EARLIER PELLING DATE: 1998-06-10
EARLIER PELLING DATE: 1998-06-10
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-06-10
EARLIER PELLING DATE: 1998-06-10
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-07-30
EARLIER PELLING DATE: 1998-07-31
EARLIER PELLING DATE: 1998-07-31 5 81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140 87 ggcgctgtgcttccgaatgaaggactcggcattgaaggtgctttatctgcataataacca 146 141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197 147 gcttctagctggagggctgcatgcagggaaggtcattaaaggtgaagatcagcgtggt 206 ccgctgcctggcatgtgtggagacagaagagggccttccctacagctggaggatgtgaa 317 ccagtgcctgtcatgtggggtg---ggggcaggagccgactctaacactagagccagtgaa 323 cattgaggaactgtacaaaggtggtgaagaggccacacgcttcaccttcttccagagcag 377 Indels 10.9%; Score 110.8; DB 4; 58.6%; Pred. No. 1e-24; live 0; Mismatches 157; ggcagagccccagccagtacagctcaccaag 471 gcctgaagccgatcagcctgtcagactcacccag 477

RESULT

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APPLICANT: John Ford
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/35801
CURRENT APPLICATION: NUMBER: US/09/348,942
CURRENT FILING DATE: 1999-07-07
EARLIER FILING DATE: 1999-04-05
EARLIER FILING DATE: 1999-04-05
EARLIER FILING DATE: 1999-04-05
EARLIER FILING DATE: 1999-04-05
EARLIER APPLICATION NUMBER: US 09/251,370
EARLIER APPLICATION NUMBER: US 09/252,591
EARLIER APPLICATION NUMBER: US 09/229,591
EARLIER APPLICATION NUMBER: US 09/229,591
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1999-01-13
EARLIER FILING DATE: 1999-07-31
EARLIER FILING DATE: 1998-07-31
EARLIER FILING DATE: 1998-07-31
EARLIER FILING DATE: 1998-07-31
EARLIER FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: US 09/099,909
EARLIER FILING DATE: 1998-06-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.9%; Score 110.8; DB 4;
58.6%; Pred. No. 1.6e-24;
iive 0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: US 09/055,010
                  Sequence 6, Application US/09348942
Patent No. 6337072
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 58.6
Matches 231; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), ORGANISM: Homo sapiens
US-09-348-942-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2648
US-09-348-942-6
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
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                                                                                                                         GENERAL INFORMATION:

APPLICANT: Pace Ann
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36238
CURRENT APPLICATION NUMBER: US/09/417,455
CURRENT PELING DATE: 1999-10-13
PRIOR FILING DATE: 1999-07-07
PRIOR PAPLICATION NUMBER: US 09/348,942
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR APPLICATION NUMBER: US 09/251,370
PRIOR PELING DATE: 1999-04-07
PRIOR PELING DATE: 1999-04-13
PRIOR PELING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: US 09/229,591
PRIOR APPLICATION NUMBER: US 09/229,591
PRIOR PELING DATE: 1999-01-13
PRIOR PELING DATE: 1999-06-17
PRIOR PELING DATE: 1999-06-17
PRIOR PELING DATE: 1999-06-15
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-19
PRIOR PELING DATE: 1998-06-15
PRIOR APPLICATION NUMBER: US 09/092,364
PRIOR PELING DATE: 1998-06-15
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 tectaacagaggettggacegeaceaaggteeceatttteetggggateeagggaggag 257
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Pred. No. 1.6e-24;
0; Mismatches 157; Indels 6;
   US-09-417-455-6; Sequence 6, Application US/09417455; Patent No. 6294655
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Best Local Similarity 58.69
Matches 231; Conservative
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US-09-417-455-6
                                                                                                              GENERAL INFORMATION:
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Gaps

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DB 4; Length 2648; Indels

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catcatggagetetatettggtgecaaggaatecaagagetteacettetaceggeggga 372
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                                                                                                                                                                                81 ggcaagatactacataattaaatatgcagaccagaaggctctatacacaagagatggcca 140
                          141 gctgctggtgggagatcctgttgcagacaactgctgt---gcagagaagatctgcacact 197 | | | | | | | | | | | | | | | | | |
                                                                                                                                                          tectaacagaggettggacegeaceaggteeceatttteetggggatecagggagggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 ggcagagccccagccagccagtacagctcaccaag 471
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                                                                                Sequence 1, Application US/08862730C
Patent No. 6063600
GENERAL INFORMATION:
APPLICANT: Fuller, Gerald M
APPLICANT: Fullers, Nelson L.
TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       STREE: Douglas C Murdock/ Bradley, Arant, Rose & White CITY: Birmingham STREE: Alabama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1710;
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HYPOTHETICAL: N
ANTI-SENES: N
ORIGINAL SOURCE:
ORGANISM: Canine peripheral blood macrophage
CELL INVE: primary monocytes
IMMEDIATE SOURCE:
LIBRARY: lambda gill cDNA
CLONE: Canine IL-Ira
FEATURE:
FRAME.KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103.4; DB 3;
Pred. No. 2.5e-22;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                             COMPOSITION SYSTEM: MICROSOFT WINDOWS SOFTWARE: WordPerfect 6.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,730C FILING DATE: 5/23/97
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1710 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                             ZIP: 35203-2736
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: open reading frame: LOCATION: 60 to 587
USCATION: 1 OTHER INFORMATION:
US-08-862-730C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.1%;
Best Local Similarity 64.3%;
Matches 155; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM compatible
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                                                      RESULT 8
US-08-862-730C-1
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                         Nelson L.
DNA Encoding Canine Interleukin-1 Receptor
Antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 103.4; DB 3; Length 1710;
Pred. No. 2.5e-22;
0; Mismatches 86; Indels 0;
                                                                          AUDRESSEE: Douglas C Murdock/ Bradley, Arant, Rose & White STREET: 2001 Park Place, Suite 1400 CITY: Birmingham STATE: Alabama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Canis familiaris
CELL TYPE: canine peripheral blood macrophage
CELL LINE: primary monocytes
IMMEDIATE SOURCE:
                                                                                                                                                                                          COUNTRY: USA
ZIP: 35203-2736
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows
                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,630C
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,730
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: open reading frame; LOCATION: 60 to 587
USCATION: 00-630C-1
           APPLICANT: Fuller, Gerald M
APPLICANT: Fuentes, Nelson L.
TITLE OF INVENTION: DNA Encodi
TITLE OF INVENTION: Antagonist
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1710 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lambda gt11 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.1%; est Local Similarity 64.3%; atches 155; Conservative
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY:
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COUNTRY:
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APPLICANT: Pan, Yang
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TILE REFERENCE: 09404/052001
UNRRHY APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 176373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DD 160498 ATGATAGGCAGAATAATGGCACCCCGAAAATGTCCCAATTCTAATCCCCCAGACCCTGTGT 160439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160438 ATATGTTACATGACATAGCAAAAGGGACTTTGCATCTGTGATTAAAGGTTAAAGCCTCTTTG 160379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 160258 AGATGGGGCTACTAGCCAAGGAATGCAGGTGGCTTCTGGAAGCTGGAAAAAGGCAA 160199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160378 AGACGCGAGAGTATCCTGGATATTGACGTGAGCCCGATGTAAATTGCAAGCGTTCTTATA 160319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 160318 TGTGAAAGAGGAAGGAGGGTCAGAGCAAAGCAGTGTGAGAAAAACCCAAGCAGGA 160259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagat-ctgtgc 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 atatgttaccatacatgtccaaagaggttttgcaaatgtgatt-atgttaaggatcttga 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 aatgaggagacaateetgggttateettgtgggeteagtttaateaeaag-----a 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            814 atggagtgaggggccttgagccaacaaatgcaggt-gtttttagaaggtggaaaagccaa 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 gggaacggattctcctctagagtctccggaaggaa--cacagctcttgacacatggattt 930
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537
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478 CCTGCCCTGGCTGCTTCCTCTGCACAGCACTGGAGGCCGACCGGCCTGTCAGCCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 176373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.5%; Score 97.4; DB 3; Length 1 Best Local Similarity 62.1%; Pred. No. 2.9e-19; Matches 259; Conservative 0; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-724-394A-20/c
; Sequence 20, Application US/08724394A
; Patent No. 5872237
                                                                                                                                                                                                                           Sequence 17, Application US/09128155
Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; GENERAL INFORMATION:
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37190 AGGGTAGGCTGAATGTTGTCCTCCAAAGATATCCATGTCCTAATCCCCAGAACCTGTAAA 37131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgca 644
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Best Local Similarity 62.1%; Pred. No. 4.7e-19;
Matches 259; Conservative 0; Mismatches 140; Indels 18;
                                       APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Touchinashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORRESPONDENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

) LOCATION: 1.246240

) OTHER INFORMATION: /note= "HLA-H.CONTIG"

US-08-724-394A-20
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01-0CT-1996
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TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Kronmal,
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37071 TGGGCAGATTTTCCTGAATTTTGCAGATGGGCCCTAGTGTAAATCACAAGGGTCCTTATAA 37012
                                                                                     37011 GAGACAGGCAGAAGAGTCAGAATAAGAGAAAAATACTTCAAGATGTTACACTGCTGGTT 36952
                                                                                                                                                                            36951 TAAGGTGGAGGAAAGGCCAAGAGCCAAAAAATGCAGTGGTCACTACAAGGT-GAAAAGAA 36893
                                                                                                                               817 gagtgagg-----ggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagcc 870
                                            757 aggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaagatg 816
                                                                                                                                                                                                                    871 aagggaacggattctcctctagagtctccggaaggaacacagc--tcttgacacatggat 928
                                                                                                                                                                                                                                                                                                         Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Megabase Transcript Map: No. 5872237el
: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB 2;
Pred. No. 4.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Tauchihashi, Zenta
APPLICANT: Tauchihashi, Zenta
APPLICANT: Wolff, Roger K.
ITLE OF INVENTION: Megabase Transcr
TITLE OF INVENTION: Sequences and An NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIF: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pa:
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MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: not r
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-724-394A-22/c
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                                                                           929 ttcagctcagtgacacccatttcagacttctgacctccacaactataaaataaa 985
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                                                                                                                                                                                      Sequence 21, Application US/08724394A
Petent No. 587237
GENERAL INFORMATION:
FAPPLICANT: Feder, John N.
APPLICANT: Feder, John N.
APPLICANT: Towns, Peter M.
APPLICANT: Thomas, Winston
APPLICANT: Towns, Winston
APPLICANT: Towns, Winston
APPLICANT: Towns, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELECHOME: 415-576-0200
TELEFA: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N: USA
94111-3834
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MOLECULE TYPE:
                                                                                                                                                  RESULT 11
US-08-724-394A-21/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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293 cttccctacagctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggcca 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 ttttcctggggatccagggaggagccgctgcctggcatgtgtggagacagaagaggggc 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413 ggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaagg 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09131247

Patent No. 6294170

GENERAL INFORMATION

APPLICANT: Hershenson, Susan

APPLICANT: Bevilacqua, Michael P.

APPLICANT: Collins, David S.

TITLE OF INVENTION: DISEASES

TITLE OF INVENTION: DISEASES
                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                           9.3%; Score 95; DB 3; Length 462; 61.5%; Pred. No. 4.8e-20; tive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 95; DB 4; Length 462; Pred. No. 4.8e-20;
                                                                                                                                                                                            /note= "Initial methionine is
optional."
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OTHER INFORMATION: Initial methionine is optional
-09-131-247-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REPERENCE: A.365F
CURRENT APPLICATION NUMBER: US/09/131,247
CURRENT FILING DATE: 1998-07
EARLIER APPLICATION NUMBER: 60/055,185
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-02-10
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                           Query Match 9.3%
Best Local Similarity 61.5%
Matches 152; Conservative
                                                                                                                                                           NAME/KEY: misc_feature
                          single
                                                                                                                                                                             ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-798-414-1
TYPE: nucles.
STRANDEDNESS: sing
          nucleic acid
                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                        1..462
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Best Local Similarity
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ORGANISM: Human
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                                                                                                                        LOCATION:
                                                                                                     NAME/KEY:
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US-09-131-247-1
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                                                                                                                                                                                                                                                                         757 aggcaggaagggagagtcagagagagagatggaagataccatgcttctaattttgaagatg 816
                                                                                                                                                                                                                                                                                                                                                   817 gagtgagg ----ggccttgagccaacaaatgcaggtgttttagaaggtggaaaagcc 870
                                                                                                                      tatgttaccatacatgtccaaagaggttttgcaaatgtgattatgttaaggatcttgaaa 704
                                                                                                                                                                                              705 tgaggagacaatcctgggttatccttgtgggctc-agtttaatcacaag-----aagg 756
                                                                                                                                                                                                                                                                                                                                                                                                                              871 aagggaacggattctcctctagagtctccggaaggaacacagc-.tcttgacacatggat 928
                                           585 atggtaggcagaataatgtcccccgaaatatgtccacatcctaatcccaagatctgtgca 644
        Gaps
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        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-798414-1
Sequence 1, Application US/08798414
Patent No. 6096728
GENERAL INFORMATION:
APPLICAMT: BUYLLACOUA, Michael P.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING
TITLE OF INVENTION: INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
        Indels
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      140;
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        Mismatches
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APPLICATION NUMBER: US 60/011,419
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,789
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 64/032,789
PRIOR APPLICATION NUMBER: US 64 DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/798,414
FILING DATE: 07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1840 De Havilland Drive CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A-365C
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               462 base pairs
    Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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OTHER INFORMATION:
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                                                     , NAME/KEY:
, LOCATION:
US-08-476-860-9
                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                              ttttcctggggatccagggaagccgctgcctggcatgtgtggagacagaagaggggc 292
                                                                                             413 ggcctggctggttcctgtgtggcccggcagagccccagcagccagtacagctcaccaagg 472
   Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PetentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
PRILING DATE: 07-JUN-1995
CLASSIFTCATION: 435
PRICA APPLICATION NUMBER: IT MI 94 A 002097
FILING DATE: 13-OCT-1994
ATTORNEY AGENT INFORMATION:
ANALE: PROGRAY
ANALE: PROGRAY
ANALE: PROGRAY
COMPUTED AND ATA:
ANALE: PROGRAY
ANALE: PROGRAY
ANALE: PROGRAY
COMPUTED AND ATA:
ANALE: PROGRAY
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   95;
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STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
   Mismatches
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: COLOTTA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: COLOTYA, Francesco
APPLICANT: MUZIO, Marta
APPLICANT: MANTOVANI, Alberto
TITLE OF INVENTION: 1L-1 ANTAGONIST
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08476860 Patent No. 5739282
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
      Matches 152; Conservative
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OTHER INFORMATION:
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-08-476-860-9
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                                                                                                                                                                                                                                       233 ttttcctggggatccagggagggagccgctgcctggcatgtgtggagacagaagaggggc 292
                                                                                                                                                                                                                                                                   353 cacgetteacettettecagageageteaggeteeggetteaggettgaggetgetget 412
                                                                                                                                                                                              Gaps
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codon in the inner region of the sequence
                                                                                                                                                   Length 474;
                                                                                                                                                   9.3%; Score 95; DB 1; Length 474
61.5%; Pred. No. 4.9e-20;
tive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 19, 2002, 08:49:59 Job time: 14498 sec
                                                                                                                                                                           Best Local Similarity 61.5
Matches 152; Conservative
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 10, 2002, 13:51:47; Search time 24.69 Seconds (without alignments) 900.502 Million cell updates/sec Run on:

Title: Perfect score:

US-09-724-583-2 818 1 MCSLPMARYIIKYADQKAL.....QLTKESEPSARTKFYFEQSW 152 Sequence:

473505 seqs, 146272329 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

473505 Total number of hits satisfying chosen parameters:

nimum DB seq length: 0 daximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_fungi:*
sp_human:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_phage:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:* sp_plant:* sp_rodent:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Ouerv	Score Match Length DB ID Description	72.4	11 Q9JIG2 Q9jig2 mus	11 Q9QYY1 mus	155 4 Q9UBНО 09ubh0 homo	159 11 070207	30.3 176 6 Q9вЕНО	177 6 Q9GMZ4	143 4 Q9UPC0 Q9UPC0	29.2 180 4 Q14628 Q14628	29.1 176 6 Q9GKK2 Q99kk2	21.7 169 4 Ф9ихнв 21.7	157 4 Q9UHA5 Q9uha5	21.0 183 11 Q9D6Z6 mus	20.7 158 4 Q9UHA7	72 6 077771	178 4 Q9HBF2 Q9hbf2	192 4 Q9UHA6 Domo	218 4 Q9NZH6 homo	
		Score	592	309	307	283	257.5	248	245	238.5	238.5	238	177.5	176	172	169	164.5	156	155.5	155.5	
•	Sult	No.	1	7	m	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	

Db δ

PRT; 156 AA.

09JIG2 PRELIMINARY; PRT; 09JIG2; 01-OCT-2000 (TrEMBLrel. 15, Created)

RESULT 2 Q9JIG2 ID Q9JIG2 AC Q9JIG2; DT 01-OCT-

20	073909 gallus gall 09j1a2 mus musculu 029082 sus scrofa 029vz5 xenopus lae 09tzj0 equus cabal 08vyg1 cavia porce 09tKl tursiops tr 09tygd3 oncorhynchu 08jpt12 oncorhynchu 043645 homo sapien 057398 cyprinus ca 057398 cyprinus ca 057398 cyprinus ca 057398 cyprinus ca 057437 equus cabal 057398 cyprinus ca 050437 cyprinus ca 050404 homo sapien 060800 mus musculu 060800 mus musculu 060800 mus musculu 060800 cyprinus ca 09tyj deinococcus 0544183 solsococus 09ddf2 cyprinus ca 09tyj	ALIGNMENTS PRT; 144 AA. Created) Last sequence update) Last sequence update) Last sequence update) Last sequence update) SOUIST FKSG75. Craniata; Vertebrata; Euteleostom1; Craniata; Vertebrata; Homo. Craniation of FKSG75, a novel member of the EMBL/GenBank/DDBJ databases. W. 8733B16D6F118BB9 CRC64;	ore 592; DB 4; Length 144; dd. No. Be-55; Mismatches 2; Indels 0; Gaps 0; CLACVETEGGSLQLEDVNIEELYKGGERATRF 99
20 1 22 1 22 2 1 22 2 1 22 2 1 22 2 1 22 2 1 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	073909 099162 029082 0297830 0997830 099781 097781 097781 097781 097781 097739 097739 097739 097739 097739 097739 097739 097739 097739 097739 097739	undz → Σ·	Score 592; Pred. No. 0; Mismatc GGSRCLACVET [[
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IL-1L1 PROTEIN (INTERLEUKIN-1 HOMOLOG 3).
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RC STRAIN=CSTBL/64; TISSUE=TONGUE, AND STOMACH;

RC STRAIN=CSTBL/64; TISSUE=TONGUE, AND STOMACH;

RAWAI J. Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa T., Saito R.,

Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Schrimin L.M., Satubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrimin L.M., Staubi F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Caribodi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita W., Stonch K.-F.,

RA Basaki H., Sato K., Schoenbach C., Saya T., Shibate Y., Storch K.-F.,

RA Basaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

REMBI, AR008977; BAB260221; Illy.

REMBI, AR008977; BAB260221; Illy.

BR BREN, AR008977; Interleukin_1.

BR BRAN, RO08977; BAB260221; Interleukin_1.

BR BRAN, RO08977; BAB260221; Illy.

BRAN, RADOTA R., RAD
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                                                                                                                                                                                                                                 "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TATERLEUKIR-1 DELTA (INTERLEUKIN 1 RECEPTOR ANTAGONIST HOMOLOG 1).
                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity 45.2%; Pred. No. 6.3e-25;
Matches 70; Conservative 23; Mismatches 56; Indels
                                                                                                                                                                                        Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
Kastelein R.A.;
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Last annotation update)
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(TrEMBLrel. 17, Last anno
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=10090;
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01-JUN-2001 (
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SEQUENCE FROM N.A.
Barton J.L., Nicklin M.J.H.;
"IL-1L1: A Novel Member of the Interleukin-1 Gene Family is Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                      Young P.R.; Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-20209405; PubMed*10744718; Kunar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
FILL DELTA (INTERLEUKIN-1 LIKE PROTEIN 1) (INTERLEUKIN-1 RECEPTOR
ANTAGONIST HOMOLOG 1) (INTERLEUKIN-1 DELTA).
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Euteleostomi,
Mammanla, Eutheria, Rodentia, Sciurognathi, Muridae, Mus. Mus.
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Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Euthheria: Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E., Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%; Score 307; DB 11; Length 155; 47.8%; Pred. No. 1e-24; tive 20; Mismatches 46; Indels
                                                                                                                                                                                                                                 in Trophoblasts and Macrophages.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AA; 17004 MW; A4B1770F2E12533A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the interleukin-1 family.'
J. Biol. Chem. 275:1038-10314(2000).
EMBL; A7260429; CAR59831.1; -
EMBL; AF200495; AAF69251.1; -
HSSP; P18310; ILR.
MGD; MGI: HS59235; Illhyl.
InterPro; IPR00975; Interleukin_1.
SMART; SM00125; III; 1.
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MEDLINE=99443727; PubMed≈10512743;
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Best Local Similarity 47.89
Matches 66; Conservative
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                                                                                     NCBI_TaxID=10090;
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Receptor
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                                                                         TISSUE-PLACENTA;
Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
A tissue specific interleukin 1 receptor antagonist homolog from the
ILI cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
At tissue specific interleukin-1 receptor antagonist homolog from the
IL-1 cluster lacks IL-1, IL-Ira, IL-18 and IL-18ra activities.";
Submitted (JAN-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 PSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
**Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF201807, AAF2510.1;
**EMBL, A7242781; CAB5982.1; -.

EMBL, A7242781; CAB5982.1; -.

EMBL, A7242781; CAB59823.1; -.

EMBL, A7242783 CAB57704.1; -.

EMBL, A721383, CAB57704.1; -.

EMBL, A7216591; AAF7681.1; -.

EMBL, A7216591; AAF7681.1; -.

EMBL, A7216591; AAF7681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALYTRDGQLLVGDPVADNCC-AEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETEEG
                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-20322477; PubMed=10865108; Mulero J.J., Nelken S.T., Ford J.E.; Moraonization of the Human Interleukin-1 Receptor Antagonist Gene LIHH1.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R., Drmanac R., Ford J.E., "ILIHY1: A Novel Interleukin-1 Receptor Antagonist Gene."; Biochem. Biophys. Res. Commun. 263:702-706(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 155;
                                                                                                                                                                                                                                                                                                                         Timans J.C., Zurawski S., Sana T.R., Bazan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49; Indels
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
INTRACELLULAR INTERLEUKIN-1 RECEPTOR ANTAGONIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 34.6%; Score 283; DB 4;
1 Similarity 45.7%; Pred. No. 3.5e-22;
63; Conservative 20; Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00253; INTERLEUKIN_1; UNKNOWN_1.
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Pfam; PF00340; IL1; 1.
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                                                            SEQUENCE FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Kastelein R.A.;
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Best Local Si
Matches 63;
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                                                                                                                                             STRAIN-FVBXDBA/I LACJ;
MEDLINE-28203757; PubMed-9550387;
Gabay C., Porter B., Fantuzzi G., Arend W.P.;
Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning and protein expression of intracellular isoform and tissue distribution of secreted and intracellular IL-1 receptor antagonist in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SI DDIKLQLEEVNITDLSKNKEEDKRFTFIRSEKGPTTSFESAACPGWFLCTTLEADRPVSL 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 NQKTFYLRNNQLIAGYLQGPNIKLEEKIDMVP---IDLHSV--FLGIHGGKLCLSCAKSG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 CRMQAFRIWDV --- - NOKTFYLRNNQLVAGYLQGSNTKLEEKLDVVPVE----- PHAVFLG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Shin I.-S., Youn H.-Y.,
"Molecular cloning of canine interleukin-1 receptor antagonist (IL-
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.3%; Score 248; DB 6; Length 176; 39.7%; Pred. No. 2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 257.5; DB 11; Length 44.5%; Pred. No. 1.7e-19; Live 16; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; AY026462; AAK01472.1; -.
                                                                                                                                                                                                                                                                                                                                                                              EMBL: ARC10255. AAC15251.1; -...
HSSP, PR8510. 11RA.
HSSP, PR8510. 11RA.
HSSP, PR8510. 11RA.
InterPort: PR000975; Interleukin_1.
Pfam; PF00340; ILI; 1.
SMART; SM00125; ILI; 1.
SMART; PS0025; INTERLEUKIN 1; 1.
SRGUENCE 159 AA: 17995 MW; A7CD35D137846222 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 159:5905-5913(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.5%
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 TK-ESEPSARTKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.3%
Best Local Similarity 39.7%
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
                                                                                                                     SEQUENCE FROM N.A.
                                                            NCBI_TaxID=10090;
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29.2%; Score 238.5; DB 4; Length 180;
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Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P18510; 1IRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                               Receptor.
NON_TER
SEQUENCE
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Q14628
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                                                                                                                                                                                                                                                                                                                                                                                                             Tursiops truncatus (Atlantic bottle-nosed dolphin).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDILINE-98183404; MEDILINE-98183404; PubMed-9514884; Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.; "Detection of an interleukin-1 intracellular receptor antagonist mRNA variant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 IHGGKLCLACVKSGDETRLQLEAVNITDLSKNKDQDKRFTFILSDSGPTTSFESAACPGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFQSSSGSAFRLEAAAWPGW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNC - CAEKICTLPNRGLDRTKVPIFLG 60
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLP.1. 17, Last annotation update)
INTERLEUKIN-1 INTRACELLULAR RECEPTOR ANTAGONIST VARIANT (FRAGMENT).
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inoue Y., Itou T., Sakai T.;
Inoue Y., Itou T., Sakai T.;
"Cloning and Sequencing of a Bottle-Nosed Dolphin Interleukin-1
"Cloning and Sequencing of a Bottle-Nosed Dolphin Interleukin-1
Seceptor Antagonist.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB038268; BAB11806.1; -.
InterPro: IPTR000975; Interleukin_1.
ProDom; PD002536; Interleukin_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE 177 AA: 19923 MW; 6FD19A06C09B131B CRC64;
                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.0%; Score 245; DB 6;
40.4%; Pred. No. 4.1e-18;
Live 18; Mismatches 62;
                                                                                                                                                                                                                                   177 AA.
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                                                   121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 FLCTALETDQPVGLTNTPQDAVQVTKFYFQQ 175
                                                                               145 FLCTALEADRPVSLTNRPEEAMMVTKFYFQK 175
                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
INTERLEUKIN-1 RECEPTOR ANTAGONIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9739;
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                                                                                                                                                                                                                                Q9GMZ4
Q9GMZ4;
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Q9UPC0;
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                                                                                                                                                                               RESULT 7
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SEQUENCE FROM N.A.

MEDLINE-3746044, PubMed=8992991,
Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
Arend W.P., Smith M.F. Jr.;
A. Immunol. 158:748-755(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 NOKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIE----PHALFLGIHGGKMCLSCVKSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-9535865; PubMed-7629520;
Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
Introna M., Mantovani A., Colotta F.;
"Cloning and characterization of a new isoform of the interleukin I
receptor antagonist.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Mismatches 56; Indels
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X84348; CAA59087.1; -.
EMBL; U65590; AAB92269.1; -.
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Pfam; PF00340; IL1; 1.
SMART; SM00125; IL1; IL.
SMORT; ES00253; ILN: IL.
SEQUENCE 180 AA: 19897 MW; 624A1574C2334229 CRC64;
                                                                                                                                                                                                                                                                                                                 143 AA; 16142 MW; 4CAD6784B890906B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTRACELLULAR IL-1 RECEPTOR ANTAGONIST TYPE II.
Biochem. Biophys. Res. Commun. 244:91-95(1998).
EMBL; AF043143; AAC39672.1; -.
HSSP; P18510; IITN.
                                                                                                                                                                                                                                                                                                                                                                                                                29.2%; Score 238.5; DB 4 40.9%; Pred. No. 1.6e-17;
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                 Pfam; PF00340; IL1; 1.
SMART; SM00125; IL1; 1.
PROSITE; PS00253; INTERLEUKIN_1; 1.
                                                                                                      InterPro; IPR000975; Interleukin_1.
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the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.6%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 KESEPSARTKF 146
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                  3;
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                                                                     75 EGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQL 134
                                                                                                                                       Gaps
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                                                 16 DQKALYTRDGQLLVGDPVADNC-CAEKICTLPNRGLDRTKVPIFLGIQGGSRCLACVETE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBL_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Campbell S.E., Nasir L., Argyle D.J., Gault E., Bennett D.,
"Canine IL-1 Receptor Antagonist cDNA Sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF216526; AAG36777.1; ...
InterPro; IPR000975; Interleukin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 176;
Local Similarity 40.9%; Pred. No. 2e-17; nes 56; Conservative 18; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 AA; 19938 MW; 8486CA54A254206B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-1 HOMOLOG 1 (INTERLEUKIN-1 EPSILON).
                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.1%; Score 238; DB 6;
Best Local Similarity 39.1%; Pred. No. 2.2e-17;
Matches 59; Conservative 20; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FLCGPAEPQQPVQLTKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 FLCTALEADRLVSLTNRPEEAMMVTKFYFQK 175
                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                           Created)
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ProDom; PD002536; Interleukin_1; 1.
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                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TIEMBLEEL 16, Created U-MAR-2001 (TIEMBLEEL) 16, Last so 01-JUN-2001 (TIEMBLEEL) 17, Last at INTERLEUKIN-1 RECEPTOR ANTAGONIST.
                                                                                                                                                                                   135 TKESEPSAR-TKFYFEQ 150
                                                                                                                                                                                                                  162 TNMPDEGVMVTKFYFOE 178
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              Canis familiaris (Dog).
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SEQUENCE
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Q9NZH8
Best Loca
Matches
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                                                                                                Young P.R.; "Identification and initial characterization of four novel members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GPSLQLEDVNIEELYKGGEEATRFTFPQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 LYTRDGQLLVGDPVADNCCAEKI ----CTLPNRGLDRTKVPIFLGIQGGSRCLACVETEE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE-AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
TISSUE-AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;
Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
"Novel IL.1 family member IL-le responds through the orphan IL-IR-
related protein 2; response is antagonized by IL-1d.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206492; AAG35670.1; -.
EMBL; AF206492; ARG35670.1; -.
EMBL; AF206492; Interleukin_1.
SMART; SM00125; ILL: 1.
MEDLINE-20209405; Pubwed=10744718;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 169;
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Sims J.E.;

"Four New Members Expand the IL-1 Superfamily.";

"Four New Members Expand the IL-1 Superfamily.";

"Substituting J.E.;

"EMBL; AR201331, AR752213.1;

"R HSSP; P10749; 2MIB.
"R InterPro: IPR000975; Interleukin_1.
"R Pfam; PF00340; ILI; 1.
"R MART; SW00125; ILI; 1.
"PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%; Score 176; DB 4; Length 15
36.6%; Pred. No. 6.8e-11;
iive 18; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.7%; Score 177.5; DB 4; Length 33.6%; Pred. No. 5.2e-11; Live 21; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 AA; 18721 MW; F00A9243706F4154 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Q9UHA7
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 RESULT
Q9UHA7
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RR SEQUENCE FROM N.A.

RAWADINE-21085660; Pubbmed-11217851;

RAWADINE-21085660; Pubbmed-11217851;

RAWADINE-21085660; Pubbmed-11217851;

RAWADINE-21085660; Pubbmed-11217851;

RAWADINE-21085660; Pubbmed-11217851;

RAWADIANE A., Stubil Y., Konno H., Adachi J., Fukuda S., Arawada T., Arawada T., Saito R., Adacha K., Izawa M., Nishi K., Kiyosawa T., Saito R., Adacha K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Rabelis C., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Rochimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rasia K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barsh G., Bolunga N., Carninci P., de Bonaldo M.F., Rawatein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rodfelli D., Bolunga N., Carninci P., de Bonaldo M.F., Rubing B., Ringwald M., Rodriguez I., Sakamoto N., Raborone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Saya T., Shibata Y., Storch K.-F., Sakani H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Rawadinaki A., Yoshida K., Hasegawa Y., Kawaji H., Rohtsuki S., Anderdia R., Havachizaki W., Roshida K., Hasegawa Y., Kawaji H., Rohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
57 IFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAA 116
                   62 VYLGIKGKDLCLFCAEIQGKPTLQLKEKNIMDLYVEKKAQKPFLFFHNKEGSTSVFQSVS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 TEEGPSLQLEDVNIEELYKGGEEATRFTFFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 QQMVWVLTGNTLTAVPASNNVKPVILSLIACRDTEFQDVKKGNLVFLGIKNRNLCFCCVE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183;
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MART; SM00125; II.; 1.
PROSITE; PS00253 INTERLEUKIN_1; UNKNOWN 1.
SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02F CRC64;
                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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29.2%; Pred. No. 2.2e-10;
Live 25; Mismatches 68;
                                                                                                                                                                                                    183 AA.
                                                                      117 WPGWFLCGPAEPQQPVQLTKESEPSARTKFYFE 149
                                                                                            :||||:
122 YPGWFIATSTTSGQPIFLTKERGITNNTNFYLD 154
                                                                                                                                                                                                                                         Created)
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MGD; MGI:1916927; 2310043N20Rik.
InterPro; IPR000975; Interleukin_1.
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164 ILTHQRGKLVNTNFYIE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29.23
Matches 40; Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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                                                                                                                                                                                                                      Q9D626;
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δλ
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82 EDVNIEELYKGGEEATRFTFPQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPS 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 QLLVGDPVADNCCAEKICTLPNRGLDRTKV----PIFLGIQGGSRCLACVETEEGPSLQL 81
                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E., Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BREED THOROUGHBRED;

Dara A.K., Thompson M.S., Paradis M.R., Alcivar-Warren A.;

"Modecular Characterization of Equine Interleukin I Receptor
Antagonist (IL-Ira) Gene.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF072476; AAC62237.1;

ESSP: P18510; IIRA.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST SECRETORY FORM (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.7%; Score 169; DB 4; Length 158
32.0%; Pred. No. 3.8e-10;
Live 23; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSEY F103.07 11KA:
INTERPROY TRYOUGHY5; Interleukin_1.
Pfam: PP00340; ILL; 1.
SEQUENCE 158; ILL; 1.
SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;
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                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FILL BESTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Four New Members Expand the IL-1 Superfamily.";
J. Biol. Chem. 275:1169-1175(2000).
BEBE: ARZO1811; ARZE5211.1;
HSSP; P18510, 11RA.
158 AA.
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NON TER
SEQUENCE 72 AA; 8215 MW; 290CC9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000975; Interleukin_1.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20092888; PubMed=10625660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
PRELIMINARY;
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SMART; SM00125; IL1; 1.
                                                                                                                                                                                                                                                          Homo sapiens (Human).
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Query Match
Best Local Similarity 51.4%; Pred. No. 4.4e-10;
Matches 36; Conservative 7; Mismatches 26; Indels 1; Gaps 1;
                                  Search completed: May 10, 2002, 13:53:45
Job time: 118 sec
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May 19, 2002, 07:54:55 ; Search time 270.73 Seconds (without alignments) 6468.632 Million cell updates/sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                  1736436 seqs, 858457221 residues
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query e Match Length DB	DB	ID	Description
1	1020	100.0	1020	22		Human interleukin-
2	1016.8	99.7	1020	22	AA170235	Interleukin-1 rece
m	991.2			22	AAA89175	Human interleukin-
4	964.4		, ,	22	AAA89176	Human interleukin-
5	964.4		•	22	AAA89178	Human interleukin-
9	699.8		٠,	22	AAA89177	Human interleukin-
7	657.6			22		Interleukin-1 rece
80	634.8			22	ABA08991	Human IL-1 delta h
σ	455.8			22	AAD11148	Human FIL-1 theta

009 099 099 720 720 780 780

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Interleukin-1 receptor antagonist related protein; IL-Ira-R; human; inhibitor; antiarthritic; antirheumatic; osteopathic; antiarialmantary; neuroprotective; antidiabetic; immunosuppressive; antileprotic; antibacterial; tuberculostatic; anorectic; metabolic; antiviral; hyperglycaemic; nootropic; antiparkinsonian; antidepressant; anticonvulsive; tranquillizer; vulnerary; antiathmatic; antipsoriatic; dermatological; cytostatic; nephrotropic; antiparemorrhagic; vasotropic; cardiant; antiatherosclerotic; antiinfertility; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                  Novel interleukin-1 receptor antagonist-related polypeptide, its fragment, variant useful for treating rheumatoid arthritis, septicemia, Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
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                                                                                              10-DEC-1999, 99US-170191P.
09-MAR-2000; 2000US-188053P.
04-APR-2000; 2000US-194521P.
10-APR-2000; 2000US-195910P.
28-NOV-2000; 2000US-0170191.
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P-PSDB; AAM50217.
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antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamoma; squamoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ss.
   gagaagatctgcatacttcctaacagaggcttggcccgcaccaaggtccccattttcctg
                                 tggttcctgtgtgtggcccggcagagccccagcagccagtacagctcaccaaggagagtgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of cDNA encoding a novel human interleukin-1 receptor antagonist-related polypeptide, IL-Ira-R (see AMM5018), which has interleukin-1 inhibitor activity. The sequence was derived from CDNA clones obtained by PCR and RACE from placenta and foetal scalp cDNA libraries. Also isolated was an IL-Ira-R variants sequence (see AM70218), which differed from the present sequence at nuclectide positions 194 and 215 (both altering the encoded amino acid sequence), and a splice variant (see CAT/0236). The invention provides IL-Ira-R polypeptides and nucleic acids, as well as selective binding agents, vectors, host cells and methods for producing the IL-Ira-R polypeptides. It also provides treatment ameliorations and methods for the diagnosis, treatment amelioration and/or prevention of diseases, disorders and conditions associated with IL-Ira-R, such as those involving immune system dysfunction, infection, weight disorders, neuronal of process and prevention of diseases, immune cells, reproductive system, and eye. The nucleic acids are useful negene therapy, gene mapping, transgenic animal breeding, and as
                                                                                                                                                                                                                                                                                                                                                                                                        Novel interleukin-1 receptor antagonist-related polypeptide, its fragment, variant useful for treating rheumatoid arthritis, septicemia, Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
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 /*tag= a
replace(194,C)
/*tag= b
replace(215,A)
/*tag= c
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2000US-194521P.
2000US-195910P.
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28-NOV-2000; 2000US-0170191
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Best Local Similarity 99.8
Matches 1018; Conservative
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                                                                                                                                                            04-DEC-2000;
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04-APR-2000;
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Length 998;

97.2**%**; 99.7**%**;

Similarity

Query Match Best Local S

BP; 271 A; 236 C; 264 G; 227 T; 0 other;

Sequence 998

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and neurodegenerative disorders. The polynucleotides are also useful for the design of hybridization probes and PCR primers, i chromosome and gene mapping, in the recombinant production of IL-1 Hy2 protein, and in the generation of antisense DNA or RNA.
                                                                                     WPI; 2001-016409/02
                                                             (HYSE-) HYSEQ INC.
      WO200071719-A1
                                                                         Ballinger DG,
                                           20-MAY-1999;
                  30-NOV-2000
                                                                                                                    diseases
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The present sequence is that of the cDNA insert of clone pIL-1HY2

(ATCC PTA-96) encoding human interleukin-1 Hy2 (IL-1 Hy2, see

AAB19923, an aAB19923), a novel member of the interleukin-1 receptor

antagonist family. The cDNA was obtained from a human foetal skin

contagonist family. The cDNA was obtained from a human foetal skin

and Sanger sequencing techniques. Sequencing of PCR products from

various cDNA libraries revealed potential polymorphisms at

nucleotides 125 (altering codon GAT to GAC, both Asp), 184

(altering codon ACA for Thr to ATA for Ile) and 205 (altering

codon GAC for Asp to GCC to Ala). 2 Alternative open reading

frames were identified. The first had an initiating ATG codon at

position 54-56 of the present sequence. However, a predicted cDNA

sequence (see AAA89118) based on IL-1 Hy2 genomic DNA contained a C

to T change that resulted in an alternative upstream initiating

methionine which extended the open reading frame. The IL-1 Hy2

polypeptides and polypuncleotides are used to treat cancers

involving elevated levels of IL-1, such as breast adenocarcinoma,

propertions, melanoma, giant cell tumours of bone, acute

myelogenous leukaemia, oral epidermoid carcinoma or squamous cell

carcinoma, and inflammatory disease mediated by interleukin-18 (all

carcinoma, and inflammatory disease mediated by interleukin-18 (all

carcinoma, thromobosis, acute pancreatitis, arthritis, vascultis,

lupus, immune complex glomerative diseases, diabetes

construction and second and degenerative diseases, diabetes

and animatory bowel disease, bone degenerative diseases, diabetes

constructions and discasse, bone degenerative diseases, diabetes

constructions and discasse, bone degenerative diseases, diabetes
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/note= "alters codon GAC (Asp) to GCC (Ala),
specifically claimed in Claim 9"
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/note= "alters codon GAT (Asp) to GAC (Asp),
specifically claimed in Claim 9"
replace(184,T)
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Cocation/Qualifiers 54..512
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                                                  ggttccaggaactcaggatctgcagtgaggaccagacaccactgattgcaggaatgtgtt 70
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                      3; Indels
Score 991.2; DB 22
Pred. No. 2.1e-290;
0; Mismatches 3;
                     993; Conservative
                      Matches
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Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor; antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone, acute myelogenous leuksemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ss. Human interleukin-1 Hy2 cDNA (first entry) /*tag= AAA89176 standard; 19-MAR-2001 Homo sapiens AAA89176; AAA89176 Key

Location/Qualifiers 422..880 ۵

WO200071719-A1

30-NOV-2000

22-MAY-2000; 2000WO-US14144.

20-MAY-1999; 99US-0316086. 10-MAR-2000; 2000US-0522964.

(HYSE-) HYSEQ INC.

Pace AM; HS, Lin Ho AS, Ford Ballinger DG,

WPI; 2001-016409/02. P-PSDB; AAB19922.

polynucleotide encoding interleukin-1 Hy2 for diagnosing, of treating disorders, such as cancers and inflammatory reventing and New isolated diseases

Claim 1; Page 145-146; 158pp; English.

The present sequence is that of CDNA encoding human interleukin-1 receptor antagonist family. The sequence was obtained following resequencing of cDNA clone plL-1Hy2 (see AAA89175), extending the sequencing of cDNA clone plL-1Hy2 (see AAA89175), extending the sequencing of cDNA clone plL-1Hy2 cDNA sequence (see AAA89178), predicted from the IL-1 Hy2 genomic DNA. contains a Ct or predicted from the IL-1 Hy2 genomic DNA. contains a Ct or predicted from the IL-1 Hy2 cDNA sequence (see AAA89178), nucleotide change at position 279, which generates an alternative upstream initiating methionine for open reading frame encoding a 200-amino acid protein (see AAB1824). IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers involving elevated levels polynucleotides are used to treat cancers involving elevated levels and real tumours of bone, acute myelogenous leukaemia, oral epidermoid carcinoma or squamous cell carcinoma, and inflammatory used to diagnose, prevent or treat shock, thrombosis, acute pancreatitis, arthitis, vascultis, lupus, immune complex pancreatitis, arthitis, vascultis, lupus, immune complex classes, bone degenerative disease, inflammatory bowel disease, bone degenerative disease, diabetes and neurodegenerative hybridization probes and PCR primers, in chromosome and gene mapping, in the recombinant production of IL-1 Hy2 protein, and in

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BP; 334 A; 350 C; 368 G; 314 T; 0 other; Sequence 1366

1351

051 aggatettgaaatgaggagacaateetgggttateettgtggggeteagtttaateacaag 1110 33 cagtgaggaccagacaccactgattgcaggaatgtgttcoctcccctgggcaagatacta
 92
 93 cagtgaggaccagaccactgattgcaggaatgtgttcoctccccatggcaagatacta
 95 cagtgaggaccagaccaccactgattgcaggaatgtgttcoctccccatggcaagatacta 451 cataattaaatatgcagaccagaaggctctatacacaagagacggccagctgctggtggg 510 212 272 512 811 gccagtacagctcaccaaggagagtgagcctcagcccgtaccaagttttactttgaaca 870 aggatcttgaaatgaggagacaatcctgggttatccttgtgggctcagtttaatcacaag 752 caaaggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgcctt 392 caggettgaggetgetgectggettggettgtteetgtgggeeggeagageeceagea 452 gayctggtagggagacaggaaactgcgttttagccttgtgcccccaaaccaagctcatcc 572 tgctcagggtctatggtaggcagaataatgtccccgaaatatgtccacatcctaatcc 632 692 872 Gaps cataattaaatatgcagaccagaaggctctatacacaagagatggccagctgctggtggg agatectgttgcagacaactgetgtgcagagaagatetgcacaettectaacagaggett gccagtacagctcaccaaggagagtgagcctcagcccgtaccaagtttactttgaaca 753 aaggaggcaggaagggagagtcagagagagaatggaagataccatgcttctaattttgaa gatggagtgagggccttgagccaacaaatgcaggtgtttttagaaggtggaaaagcca aagatctgtgcatatgttaccatacatgtccaaagaggttttgcaaatgtgattatgtta gctcagtgacacccatttcagacttctgacctccacaactataaaataataaacttgtgt 0; Length 1366; Indels 22; Score 964.4; DB 22; Pred. No. 3.4e-282; 0; Mismatches 6; Query Match 94.5 Best Local Similarity 99.4 Matches 968; Conservative tattgtaaacctct 1006 391 63 153 333 691 393 513 871 573 931 453 633 693 873 933 1291 993 QQ qq ò ò Db δy pp Db q Ω Qy ö QQ δ QΩ δy Db Óλ qq ōλ QQ δ g qq pp δy qq q QQ Q ò ŏ

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diseases, diabetes and neurodegenerative disorders. The polynucleotides are also useful for the design of hybridization probes and PCR primers, in chromosome and gene mapping, in the recombinant production of IL-1 Hy2 protein, and in the generation
                                                                                                                                                                                                                                                                                                                                                                   antisense DNA or RNA
                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                             WO200071719-A1
                                                                               Homo sapiens
                             19-MAR-2001
                                                                                                                       30-NOV-2000
                                                                                                                                                                                                       diseases
                   AAA89178;
                                                                                         Key
    AAA89178
RESULT
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The present sequence is that of CDNA encoding human interleukin-1 Hy2, see AAB1924), a novel member of the interleukin-1 Hy2 (IL-1 Hy2, see AAB1924), a novel member of the interleukin-1 Hy2 (IL-1 Hy2 genomic DNA (see AAB9177). It contains thymidine at IL-1 Hy2 genomic DNA (see AAB9177). It contains thymidine at ucleotide 279, whereas IL-1 Hy2 CDNA obtained by PCR amplification at nucleotide 279, whereas IL-1 Hy2 CDNA obtained by PCR amplification cotes a L52-amino acid protein, while the amplified CDNA recodes a 152-amino acid protein, while the amplified CDNA encodes a 152-amino acid protein, while the amplified CDNA controlled the resent sequence are more similar to the Kozak translation start site consensus than the sequences surrounding nucleotide 422 of the present sequence are more similar to the Kozak translation carried that IL-1 Hy2 polypeptides and polymocleotides are used to treat concers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of adenocarcinoma, brain tumours, melanoma, giant cell tumours of sequences cell carried levels of IL-1, such as breast adenocarcinoma, and inflammatory disease mediated by interleukin-18 (all claimed). They can also be used to diagnose, inflammatory bowel disease mediated by a cell damage, allograft and xenograft transplantation, graft versus constants and neutrodeconses. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosin preventing and treating disorders, such as cancers and inflammatory dispages -
                                                                                                                                                                                                                                                                                                                                                                               Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor; antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antiinflammatory; diagnosis; therapy; chromosome 2; ss.
                                                                                                                                                                                                                                                                                                                   Human interleukin-1 Hy2 cDNA (alternative ORF).
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278..880
/*tag= a
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                                                                         ВР
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                                                                             AAA89178 standard; cDNA; 1366
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10-MAR-2000; 2000US-0522964.
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P-PSDB; AAB19924.
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                                                       Gaps
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                                   Length 1366;
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0
                                                       Indels
       Sequence 1366 BP; 334 A; 349 C; 368 G; 315 T; 0 other;
                                     22;
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                                     Score 964.4; DB 22
Pred. No. 3.4e-282;
); Mismatches 6;
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                                     94.5%;
99.4%;
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Best Local Similarity 99.4
Matches 968; Conservative
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68.68;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing, preventing and treating disorders, such as cancers and inflammatory diseases -
                                                                                                        Interleukin-2 Hy2; IL-1 Hy2; human; interleukin-1 receptor; antagonist; cancer; breast adenocarcinoma; brain tumour; melanoma; myeloma; giant cell tumour of bone; acute myelogenous leukaemia; oral epidermoid carcinoma; squamous cell carcinoma; inflammation; antitumour; antiinflammatory; diagnosis; therapy; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of human genomic DNA encoding interleukin-1 Hy2 (IL-1 Hy2, see AAB19924), a novel member of the interleukin-1 receptor antagonist family. The DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pace AM;
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/note = "contains introns"
1911..2363
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                                                                                                                                                                        Location/Qualifiers
                                               BP.
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                                             AAA89177 standard; DNA; 5445
                                                                                          Human interleukin-1 Hy2 gene
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/number = 1
2364..3924
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10-MAR-2000; 2000US-0522964.
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/number = 2
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/number = 3
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3925..4011
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                                                                            19-MAR-2001
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                              RESULT
AAA89177
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cobtained by screening a commercial human BAC library with IL-1 Hy2
CDNA. Exons were predicted using GenScan software. The predicted
CDNA (see AAA89178) based on this genomic sequence contains thymidine
at nucleotide 279, whereas IL-1 Hy2 CDNA obtained by PCR
amplification (see AAA89176) contains cytosine at this position. The
change in nucleotides extends the IL-1 Hy2 Open reading frame in the
3' direction, resulting in a 200-amino acid polypeptide, whereas the
camplified cDNA encodes a 152-amino acid polypeptide (see AAB19922).
IL-1 Hy2 polypeptides and polynucleotides are used to treat cancers
involving elevated levels of IL-1, such as breast adenocarcinoma,
continumnus, melanoma, giant cell tumours of bone, acute
myelogenous leukaemia, oral epidermoid carcinoma or squamous cell
carcinoma, and inflammatory disease mediated by interleukin-18 (all
carcinoma, and carcinoma shoot used to diagnose, prevent or treat
shock, thrombosis, acute pancreatitis, arthritis, vasculitis,
lupus, immune complex glomereatitis, arthritis, vasculitis,
allograft and exenograft transplantation, graft versus host disease,
inflammatory bowel disease, bone degenerative diseases, diabetes
and neurodegenerative disorders. The polynucleotides are also
carcinoma, and mannafun in the programming production of contents or characteriors of contents or characteriors of contents or characteriors of contents of contents or characteriors.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome and gene mapping, in the recombinant production of IL-1 Hy2 protein, and in the generation of antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 5445;
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Pred. No. 1.6e-201;
0; Mismatches 7;
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uveitis, eczema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel interleukin-1 receptor antagonist-related polypeptide, its fragment, variant useful for treating rheumatoid arthritis, septicemia, Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
                                                                                                                                                                                                                                                                                                 Interleukin-1 receptor antagonist related protein; IL-Ira-R; human; inhibitor; antiarthritic; antirheumatic; osteopathic; antiarthritic; antirheumatic; osteopathic; antiinflammatory; neuroprotective; antidabetic; immunosuppressive; antiportic; antibacterial; tuberculostatic; anorectic; metabolic; antidepressant; anticonvulsive; tranquillizer; vulnerary; antidepressant; antisorialic; dermatological; cytostatic; nephrotropic; antihaemorrhagic; vasotropic; cardiant; antiatherosclerit; antinfertility; ophthalmological; gene therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and methods for producing the IL-1ra-R polypeptides. It also provides pharmaceutical compositions and methods for the diagnosis, treatment, amelioration and/or prevention of diseases, disorders and conditions associated with IL-1ra-R, such as those involving immune system dysfunction, infection, weight disorders, neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of cDNA encoding a splice variant (se AAMS0219) of human interleukin-1 receptor antagonist-related polypeptide IL-1ra-R, a novel protein that has interleukin-1 inhibitor activity. The sequence was obtained from a human placenta cDNA library by PCR amplification. The splice variant may arise from splicing (or a fusion) of the first 2 exons of the upstream IL-1 omega gene onto the second exon of the IL-1ra-R gene. The invention provides IL-1ra-R polypeptides and nucleic acids, as well as selective binding agents, vectors, host cells
                                                                                                                                                                                                                                                                      Interleukin-1 receptor antagonist related protein splice variant
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09-MAR-2000; 2000US-188053P.
04-APR-2000; 2000US-194521P.
10-APR-2000; 2000US-195910P.
28-NOV-2000; 2000US-0170191.
                                                                                                                                                     AAI70236 standard; cDNA; 744
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P-PSDB; AAM50219.
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dysfunction, lung, skin, kidney, bone, vascular system, tumour cells, reproductive system, and eye. The nucleic acids are useful in gene therapy, gene mapping, transgenic animal breeding, and as
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                                                                                                Sequence 744 BP; 183 A; 194 C; 205 G; 162 T; 0 other;
                                                                                                                                                       DB 22;
                                                                                                                                                     Score 657.6; DB 22
Pred. No. 3.6e-189;
0; Mismatches 4;
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                                                                                                                                                     64.5%;
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                                                             probes and primers.
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bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; Immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiluleer; ss.
inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; sthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 686; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                    05-FEB-2001; 2001WO-US03800
                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0496914
27-APR-2000; 2000US-0560875
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                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABB11747
                                                                                                                                                                                                         40200157188-A2.
                                                                                                                                                                               Homo sapiens.
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Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides.

CC antibodies against the polypeptides, methods of identifying compounds which be not polypeptides of the invention. Although novel, many of the cc polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence cc potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell contential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell contential therapeutic activities; stem cell growth factor activity; immunomodulatory activity; tissue growth activity; chemotactic or chemokinetic activities, nemostatic, thrombolic or thrombolytic activities; receptor or ligand activities; or may be contented in oncogenesis, receptor or ligand activities; or may be continued on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cronicary heart disease.

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cronicary heart disease.

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal creating for nucleic acids encoding them) may be used to promone conditions are perpar (or nucleic acids encoding them) be used to promone to viral, conditions and dilects), while those with an fungal infections in addition to immune disorders to plants, in consist or many activities that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a CDNA encoding a novel human polypeptide of the invention. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells

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                                             Length 827;
                                           Score 634.8; DB 22; Length
Pred. No. 3.2e-182;
); Mismatches 169; Indels
          Seguence 827 BP; 164 A; 175 C; 192 G; 129 T; 167 other;
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79.0%;
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                                           Query Match
Best Local Similarity 79.0°
Matches 636; Conservative
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NOVX; transmembrane protein; NOVTRAN; neuromedin peptide; NOVNEUR; gonadotropin-like protein; NOVGON; interleukin-l: NOVINTRA; human; eytostafic; neuroprotective; reproductive, antiinflammatory; cancer; antibacterial; cerebroprotective; antidiabetic; antiarthritic; antiathmatic; antiallergic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human interleukin-1 receptor antagonist (NOVINTRA A) encoding cDNA
tacacaagagatggccagctgctggtgggagatcctgttgcagacaactgctgtgcagag
                                                                                                                                                                                                         244 atccagggagggagcgctgcctggcatgtgtggagacagaagagggccttccctacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                 tacacaagagatggccagctggtgggagatcctgttgcagacaactgctgtgcagag
                                                                                                                                181 atccagggagggagccgctgcctggcatgtgtggagacagaagaggggccttccctacag
                                                                                                                                                                                                                                                                                                                   304 ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc
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990x-0169866.
990x-0169886.
990x-0170252.
2000us-0170252.
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05-DEC-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated FIL-1 theta polypeptide to induce or inhibit the induction of fever and to stimulate the immune system for the treatment of microbial infections \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to interleukin-1 (IL-1) family ligand designated polypeptides and nucleic acid molecules encoding such polypeptides. FIL-1 theta DNA is used to identify glaucoma, insulin dependent diabetes mellitus, ectodermal dysplasia, T-cell leukaemia/ lymphoma, wrinkly skin syndrome and tibial muscular dystrophy. FIL-1 theta polypeptides are used to activate and/or inhibit the activation of vascular endothelial cells and lymphocytes; the induction of local tissue destruction and fever; the stimulation of macrophages and vascular endothelial cells to produce IL-6 and the induction of prostaglandins. They are also used to treat inflammation and microbial therapy. The present sequence is a DNA encoding human FIL-1 theta full-length protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atgtgttccctccccatggcaagatactacataattaaatatgcagaccagaaggctcta 123
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                                                                                                                                                                                                                                                                                                                   "Human FIL-1 theta full-length protein"
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44"
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51"
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/note= This polymorphism results in an amino
acid change from Thr to Ile at position 44"
replace (131..132, TC)
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/note= "This polymorphism results in an
acid change from Thr to lle at position
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1..459
/*tag= a
/product= "Human FIL-
Human FIL-1 theta full-length DNA
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2000US-0195962,
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P-PSDB; AAE05840.
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11-APR-2000;
                                                                                                                                                                                     Homo sapiens
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the invention provides novel polypeptides (NOVX) selected from human transmembrane protein (NOVTRAN), neuromedin peptide (NOVDRUR).

Cranadomist protein (NOVTRAN), neuromedin peptide (NOVBER), and and two interleukin-1 receptor antagonist proteins (NOVTRAN A and B). The invention also provides methods in which a NOVX polypeptide, polynuclectide and antibody are used in the detection, prevention and treatment of a broad range of pathological states. NOVTRAN can be used to treat is a cell signaling disorder such as cancer, immune response disorder, hematopoistic disorder, auscle disorder, neurologic disorder, cancers of central nervous system, breast, colon, ovary, kindey, prostate and thyroid. NOVGON can be used to treat reproductive development disorder, metabolic function disorder and melanoma. NOVINTRA A and B can be used to treat bone metabolism or structure disorder, inflammatory response disorder, immune requiation disorder, septic shock, stroke, diabetes, arthurnant and concert processents a cDNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated human transmembrane, neuromedin peptide goandotropin-like protein and interleukin-1 receptor antagonist proteins, useful for treating cancer, immune response disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 412; DB 22; Length 483;
Pred. No. 1.1e-114;
0; Mismatches 10; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 483 BP; 114 A; 134 C; 138 G; 97 T; 0 other;
                                                                                         Claim 8; Fig 9A; 138pp; English.
                                       proteins, useful for treating
metabolic function disorders
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449; Conservative
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                           Interleukin-1 family ligand; FIL-1 theta; IL-1; glaucoma; leukaemia; insulin dependent diabetes mellitus; lymphoma; microbial infection; ectodermal dysplasia; wrinkly skin syndrome; antisense therapy; tibial muscular dystrophy; inflammation; gene therapy; mouse; ds.
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Pred. No. 2e-101;
0; Mismatches 106; Indels 0;
                                                                                                                                                                              /*tag= a
/product= "Mouse FIL-1 theta protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 538 BP; 132 A; 148 C; 140 G; 118 T; 0 other;
                                                                                                                                           Location/Qualifiers
29..487
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80.3%;
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2000US-0195962.
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Best Local Similarity 80.3
Matches 432; Conservative
Mouse FIL-1 theta DNA
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11-APR-2000;
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04-APR-2000;
10-APR-2000;
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                                                              protein.
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          301 gggaggtgaacaaccacccgtttcacctttttccagagaagcttgggatctgccttcag
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                                         aggtggtgaagaggccacacgcttcaccttcttccagagcagctcaggctccgccttcag
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"CDS does not include start codon"
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11-APR-2000; 2000US-0195962.
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P-PSDB; AAE05839.
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of vascular endothelial cells and lymphocytes; the induction of local tissue destruction and fever; the stimulation of macrophages and vascular endothelial cells to produce IL-6 and the induction of prostaglandins. They are also used to treat inflammation and microbial infections. FIL-1 theta DNA is useful in antisense therapy and gene therapy. The present sequence is a DNA encoding human FIL-1 theta
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                                                                                                                                                                                                                                                              Sequence 339 BP; 73 A; 96 C; 102 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   Score 335.8; DB 22;
Pred. No. 1.2e-91;
0; Mismatches 2;
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2000US-188053P.
2000US-194521P.
2000US-195910P.
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99.48;
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Best Local Similarity 99.4
Matches 337; Conservative
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                                                                                                                                                                                                                                  The present sequence is that of the coding region of CDNA encoding a novel murine interleukin-1 receptor antagonist-related polypeptide, Lira-R (see AAMSO220), which has interleukin-1 inhibitor activity. The cDNA was obtained from a day 7 mouse embryo cDNA library. The mouse IL-Ira-R gene sequence was also determined (see AAI70238). The invention provides mouse and human IL-Ira-R polypeptides and nucleic acids, as well as selective binding agents, vectors, host calls and methods for producing the IL-Ira-R polypeptides. It also provides pharmaceutical compositions and methods for the diagnosis, treatment, amelioration and/or prevention of diseases, disorders and conditions associated with IL-Ira-R, such as those involving immune system dysfunction, infection, weight disorders, neuronal dysfunction, lung, skin, kidney, bone, vascular system, tumour cells, reproductive system, and eye. The nucleic acids are useful in gene therapy, gene mapping, transgenic animal breeding, and as
                                                                                                                                   Novel interleukin-1 receptor antagonist-related polypeptide, its fragment, variant useful for treating rheumatoid arthritis, septicemia, Parkinson's disease, epilepsy, cystic fibrosis, Paget's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 328.4; DB 2
Pred. No. 2.5e-89;
0; Mismatches 81
                                                           Bass MB,
                                                           Xia M,
                                                                                                                                                                                                               Claim 1; Fig 7; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.2%;
82.3%;
                                                           SX,
28-NOV-2000; 2000US-0170191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 82.3
Matches 377; Conservative
                                                           Ψ
                                                                                        WPI; 2001-648140/74.
P-PSDB; AAM50220.
                                                           Giles J,
                              (AMGE-) AMGEN INC.
                                                                                                                                                                                  uveitis, eczema
                                                           Saris CM,
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The present sequence is that of mouse cDNA encoding interleukin-1 Hy2 (IL-1 Hy2, see AAB1925), a novel member of the interleukin-1 receptor antagonist family. The sequence is predicted from isolated IL-1 Hy2 perpendices in predicted from isolated IL-1 Hy2 people and the predicted mouse and human (see AAB1912) IL-1 Hy2 prolypeptides share B1.7% homology. The multine apenomic DNA can be used to generate transpenic animals which overexpress IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out. Human IL-1 Hy2 protein or have the IL-2 Hy2 gene knocked out. Human IL-1 Hy2 propeptides and polynucleotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of bone, acute myelogenous leukaemia, oral epidemonid carcinoma or squamous cell carcinoma, and inflammatory disease mediated by interleukin-18 (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide encoding interleukin-1 Hy2 for diagnosing, preventing and treating disorders, such as cancers and inflammatory diseases -
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Pred. No. 2.5e-89;
0; Mismatches 81; Indels 0;
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AAA89180 standard; cDNA; 459
                                                                                                                                                                                                      Mouse interleukin-1 Hy2 cDNA.
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82.3%;
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10-MAR-2000; 2000US-0522964.
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Best Local Similarity 82.3
Matches 377; Conservative
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          ttcctgtgtggcccggcagagcccagcagcagcagtacagctcaccaaggagagtgagccc
                                   ctggaggatgtgaacattgaggaactgtacaaaggtggtgaagaggccacacgcttcacc
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10-MAR-2000; 2000US-0522964.
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                                                       The present sequence is that of mouse genomic DNA encoding interleukin-1 Hy2 (IL-1 Hy2, see AAB19925), a novel member of the interleukin-1 receptor antagonist family. The DNA was obtained by screening a commercial mouse BAC library with IL-1 Hy2 cDNA. Exons were predicted using GenScan software. The mouse and human (see AAB19922) IL-1 Hy2 polypeptides share 81.7% homology. The genomic CC DNA can be used to generate transgenic animals which overexpress CC IL-1 Hy2 polypeptides and polymouteotides are used to treat cancers involving elevated levels of IL-1, such as breast adenocarcinoma, brain tumours, melanoma, giant cell tumours of bone, acute carcinoma, and inflammatory disease mediated by interleukin-18 (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 gaataatg-tcccccgaaatatgtccacatcctaatcccaag-atctgtgcatatgttac 552 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 | 11111 |
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.larity 74.3%; Pred. No. 3.9e-51;
Conservative 0; Mismatches 96; Indels 2;
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Example 9; Page 149-151; 158pp; English.
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Job time: 5526 sec
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